SEQ ID NO: of full-	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
or ruii-	NO: of full-	of contig	NO:	docket number_	NO:in
nucleotide	length	nucleotide	of contig	corresponding	U.S.S.N.
secuence	peptide	sequence	peptide	SEO ID NO: in	09/488,725
seducuca	sequence		sequence	priority	
1734	3520	5306	7092	application 784CIP2D 82	
1735	3521	5307	7093	784CIP2D 82	9857
1736	3522	5308	7094	784CIP2D 83	10010
1737	3523	5309	7094		10011
1738	3524	5310	7096	784CIP2D 85 784CIP2D 86	10052
1739	3525	5311	7096	784CIP2D_86	10057
1740	3526	5312	7098	784CIP2D 89	10085
1741	3527	5313	7099	784CIP2D 89 784CIP2D 90	10139
1742	3528	5314	7100	784CIP2D 90 784CIP2D 92	10142
1743	3529	5314	7100	784CIP2D 92 784CIP2D 93	10165
1744	3530	5316	7101	784CIP2D_93	10173
1745	3531	5316	7102	784CIP2D_94	10173
1746	3532	5318	7103	784CIP2D 95	10273
1747	3533	5319	7104		3121
1748	3534	5319	7105	784CIP2E 2	3628
1749	3535	5321	7106	784CIP2E_4	3673
1750	3536	5322		784CIP2E_5	4018
1751	3536	5322	7108 7109	784CIP2E_6	4467
1752	3538	5323	7110	784CIP2E_7	4865
1753	3539	5325		784CIP2E_8	4916
1754	3539	5325	7111	784CIP2E_9	4923
1755	3541	5326		784CIP2E_10	4926
1,756	3542	5327	7113	784CIP2E_11	4962
1757	3542	5328	7114	784CIP2E_12	4963
1758	3543	533C	7115	784CIP2E_13	4964
1759	3544	5331	7116 7117	784CIP2E_14	4988
1.760	3546	5332		784CIP2E_15	5835
1761	3546	5332	7118	784CIP2E_16	7682
1762	3548	5333	7119	784CIP2E_17	7682
1763	3549	5335	7120 7121	784CIP2E_18	7699
1764	3550	5336	7121	784CIP2E_19	7707
1765	3551	5337	7122	784CIP2E_20	7707
1766	3552	5338	7123	784CIP2E_21	7752
1767	3553	5339	7124	784CIP2E_22 784CIP2E_23	8357
1768	3554	5340	7125	784CIP2E_23 784CIP2E_24	9065
1769	3555	5341	7126	784CIP2E 24	9324
1770	3556	5342	7128	784CIP2F_1 784CIP2F_2	2976
1771	3557	5343	7128	784CIP2F 2	3559
1772	3558	5344	7129	784CIP2F_3	4021
1773	3559	5345	7130	784CIP2F 4	4474
1774	3560	5346	7132		4566
1775	3561	5346	7132	784CIP2F_6	4705
1776	3562	5347	7133	784CIP2F_7 784CIP2F_8	4707
1777	3563	5349	7134	784CIP2F 8 784CIP2F 9	4712
1778	3564	5350	7135	784CIP2F_9 784CIP2F_10	5008
1779	3565	5350	7136	784CIP2F 10 784CIP2F 11	5009
1780	3566	5352	7137	784C1P2F_11 784C1P2F_12	5015
1781	3566	5352	7138		5015
1782	3568	5353		784CIP2F_13	7724
1783	3569		7140	784CIP2F_14	7725
	3569	5355 5356	7141	784CIP2F_15	8828
				784CIP2F 16	8830
1784					
1784 1785 1786	3570 3571 3572	5357 5358	7142 7143 7144	784CIP2F 17 784CIP2F 18	9739 9896

TRADOCS:1416247 1(%CS7011.DOC)

TABLE 7

	DLE /		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L-Leucine; M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion.
î .	sequence	Doquemoc	\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPONLSVLSTNMKHLLAWSPVIAPG
3333	337	1131	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
Į.	I	1	
			TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
	i		TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
Į.	1	1	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
1	1)	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
			KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
ł	1		CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
ļ.	1	j .	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
			FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGOKF
		l .	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
}	ı	i	FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
Į.		ł	GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
			AALSAGPGVGLCEEHGSPAAPOHLLGPGPVAGPKLYPKLYTGHS
			TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
0001	1	1 223	SSKHLWYMPEBYIROGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
[1	ſ	AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
Í	1	l	PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
			SQSEVMPLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
			LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
		1	NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
1	1	l	VSPPIFPAHLASVSTFLLSSMESVINPNITSQDKNEQGGMLCSQ
			MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
1			FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
!	1	1	VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1		1	RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1	į .		EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
1			PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSOEGSEIIIOAL
			ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
l .			TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
1 .			GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
I .			ASKRRKEVAPPLIAPNASONLVTSDLTTMGLIAKSVEIPTTNLH
1			SNVIPTCEPOSLVENLTOKLNNVNNOLFWIDVKENFKTSLESHT
1 .			
			VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
1			LBIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
1			QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1			MINIQFNDKVNKPFVCQNQGCNYSANTKDALFKHYGKIHQYTPE
			MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
i i			EBMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
1			PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
			EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFFTRY
1	i l		SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1			HEMTPEEIESMFASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD
1	l l		HGIGLRASKTERDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
1			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
1			KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
[]	į į		DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
			TSOHRNLLIVFKRCCNSOVKETSEOEGAKNDVKDSDTCVSESND
1			NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
[]		J	NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
		*	KAEPASAAELSSVRKEEETAVAIOTIEEHPASPDWSSFKPMGFE
			VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL

ID beginning mcleotide No: nucleotide corresponding to first arino acid anino acid residue of arino acid sequence corresponding to first arino acid anino acid arino acid sequence corresponding to first arino acid arino acid arino acid sequence corresponding to first arino acid arino acid sequence corresponding to first arino acid arino acid sequence corresponding to first arino acid sequence corresponding to the first acid acid acid acid acid acid acid acid	de
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amino acid sequence Codon, /-possible nucleotide deletion. 5363 8066 703 RUEGOLERNETPUSIKKLESUNISNETHSONINGEN 516RATGRED VIENCLERNETPUSIKKLESUNISNETHSONINGEN 516RATGRED FRENKENPORTERLERANDEN LICETPUSIFER PERPETER FRENKENPORTERLERANDEN LICETPUSIFER PERPETER GENERALDEN LICETPUSIFER LI	go
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\$363 8066 703 RLCCTSGGBOTFORASCKRAGPARTSLIVLCTPSYPPFYPFYFY PROPROPORE CREDETED PSRINERSRAMMYCLLEVIRLSLEHRLIN ROFORDILLIAN/LLCTATVPTCASKSKRAGAQVWQCOGSVAV QSKRCYTDNIKATGU TONQMENTILLANIAVCTCVTSASSGRAGE PARBOT PDINTYGNITRAVODTYREP KODMINOCTCIGAGORGA CTIANCLEGOGGS VILIGOTWARE PROTOVALECVCLGINGKORP CRI LARKCHEGOGGS VILIGOTWARE PROTOVALECVCLGINGKORP CRI LARKCHEGOGGS VILIGOTWARE PROTOVALECVCLGINGKORP CRI LARKCHEGOGGST VILIGOTWARE PROTOVALECVCLGINGKORP ENKLESHITSVQTTS SOGSOFTUVRANTO QUPROP PTIAVC GONGORO VILIGOTHORA ORGANIZACI QUPROP TIAVC GONGORO VILIGOTHORA ORGANIZACI QUPPLIVANTICUS CONSIDERATION CONTROLLED CONSIDERATION CONTROLLED CONSIDERATION CONTROLLED CONTROLLE	
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PPSWREQPPGGTENPERSELREAMUNTCLT/WFAS_LEHLAND ROPGGTGLLAND.CLCTAMPPGTGAS.KERRAGO,NOWLOGSPVAN GSKRGCYDBCKATCGLAND.CLCTAMPPGTGAS.KERRAGO,NOWLOGSPVAN GSKRGCYDBCKATCGLAND.CLCTAMPGTGAS.KERRAGO,NOWLOGSPVAN GSKRGCYDBCKATCGLAND.CLCTAMPGTGAS.CLCTAMPGTGAS. PARABETC PDSTATCTTAMPGTTSTERPCOMMENTATCGLANGESSE PARABETC PDSTATCTTAMPGTGASTAMPGTGAAMPG	WP
REFERENCIALIAN/ILLITA/PETASIS/REAQA/VYOLES/YWA QSIS/COTIONALIAN/ILLITA/PETASIS/REAQA/VYOLES/YWA QSIS/COTIONALIAN/ILLITA/SIS/COTIONALIAN/ILLITA/SIS/SIS/COTIONALIAN/ILLITA/SIS/SIS/COTIONALIAN/ILLITA/SIS/SIS/COTIONALIAN/ILLITA/SIS/C	ML
PRESET PRIVINGNITHANGITHER MOMINION COLORAGES. CITLANGEREGORY KILOTHANGITHER TOWNLEVCULGHOKUSE CITLANGEREGORY KILOTHANGITHER TOWNLEVCULGHOKUSE CITLANGEREGORY KILOTHANGITHER TOWNLEVCULGHOKUSE CITLANGEREGORY AND COLORAGE ENCERNITHANGITHER STEEDSTON COLORAGE ENCERNITHANGIT	
CTIANCCHEGOGYKICOTWREPERTOGYMLECVCLONKORE CEP LARKCPHANATSYVUGETWEPKPGOMYMCTCLICLEGES LTCTSRNCKHODTRTSYKIOTWRSKKONROKLLOCTCONSO BWKCEMHTSVGTTS-SEGSEPTUTANTYOPOHPOPPTGHCC DSGVVTSVGHQLA-KTOGKHOLLOCTLGROWSOGETATOTY GISNGBEVLIP-PTHICATPTSCTEREQDGHIMCSTTSHYEQI KTSCTHTVLATPROGRISHALICLEFTHINTTOTSGS DININKGOTTONDADLKSPGTWALEELEICTTSRGVTHEGOG DKGHMSGTCTVGTRGSBWTCLTAYSGLROCTVDLTTSHGD DKGHMSHORTCTVGTRGSBWTCLTAYSGLROCTVDLTTSH DTFHKHBEGHMANCCTGVGGROWSEDYTTYV DTFHKHBEGHMANCCTGVGGROWSEDYTTVGTWGTD	SK
CEP LABECEPHAADTSYVUSETMEREPYGGMWYDCTCLEGGS ITCTSHRICENDDTFFS YELDOWSKOMBOOLDGCLEGGSS ITCTSHRICENDDTFFS YELDOWSKOMBOOLDGCLEGGSS EWCEMHTSVQTTS SGSSFTUVRAAVYGDGPHGPPFTSHCT BOSQVVTS VGGGLAF KYGGGKGMLAFCCLEGGWSTGGETHGF GRSSGBFVLPFTJIGHTFSCTTERERDGHINGSTTSHTSGT GRSSGBFVLPFTJIGHTFSCTTERERDGHINGSTTSHTSGT GRSSGBFVLPFTJIGHTFSCTTERERDGHINGSTTSHTSGT GRSGGBFVLPFTJIGHTFSCTTERERDGHINGSTTSHTSGT GRSGGBFVLPFTJIGHTFSCTTGGBFVLTAGGT GRSGGBFVLTAGGFT GRSGGBFT GR	RIS
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DSGVVYSVGNGLA-KTOGKKOML\GTGLGKVSGGETANTOTY GISHGBEGU-PFTHIGHTPYSCTERGDGHHLGGTFSGFEG KTSCTHITVLATPRGGRISHGALGHFFFLXINHNITTOCTSGG DINKKGTTONDADGKSFGFWALGHEI GTTRSGVTFSGG DINKKGTTONDADGKSFGFWALGHEI GTTRSGVTFSGG DKGHSHGHRGTGVGNGSBKTGLAYSGLRDGCTVDLTTNI DFFHKHBEGHMAGTGFGGGGRISHGTLAYSGLRDGTVDLTTNI DFFHKHBEGHMAGTGFGGGGRINGTPDTGDGSSTTFYG	
KY SPCTHTVLVQTRAGASNAALCHE PPLINNINTTOTS ISO DINNINGCTTON/DADQKEPCTWAALIEE LCTTMSEVITYI IGO DKQHUMSHHMRCTCVONGREBHTCLTAYGLROCUTVDITTYN DFFHKHREBERHMCTCTGYGGRKEKCTWYGGDS ENTOF FY	
DNMKCCTTONTDADOKROFCPMAAHEE ICTTNEGWAYN ICDC DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYD DTPHKRHBGCHMLKCTCFGQGRGRKKCDFWDCQDSENGTFY	DQ
DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYN\ DTFHKRHBEGHMLNCTCFGQGRGRNKCDPVDQCQDSETGTFYQ	RR
DTFHKRHBEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFY(OW
DTFHKRHBEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFY(WW
TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEAT:	IP
GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTS	ST
PVTSNT\VTGETTFFSPLVATSESVTEITASSFVVSWVSASD1)TV
SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIV	VN
VYQISEDGEQSLILSTSQTTAPDAPPDFTVDQVDDTSIVVRWS	
PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQ\	MY
ITIYAVEENQESTFVVIQQETTGTPRSDTVPSPRDLQFVEVTI	
KVTIMWTPPESAVTGTRVDVIPVNLPGEHGQRLPLSRNTF\AI	
TGLSPGVTYYFKVFAVSHGRESKPLTACQTTKL\DAPTWLQF\	
ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSI	
PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPY	
TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGS1	
VSGLTPGVEYVYT1QVLRDGQERDAP\IVNK\VVTPLSPPTNI	
LEANPDTGVLTVSWERSTTPDITGYRITTFTNGQQGNSLEEV	
HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPA	
PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKt	
GRMLQSLSIFFLSUN\AVVLTNLLPGTEYVVSVSSVYEQHEST	
\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TI	
TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEY\	
SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\Sv	
APAVTVRYYRITYGRTGGNSPVQEFTVPGSKSTATISGLKPG\	
YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDN	
ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEW	
EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTI	
DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDT BLOGLRPGSEYTVSVVALHDDMESOPLIGTOSTAIPAPTDLKE	
BEQGERPGSEYTVSVVALHDDMESQPLIGTQSTALPAPIDLKE QVTPTSLSAOWTPPNVOLTGYRVRVTPKEKTGPMKEINLAPDS	
QVTPTSLSAQWTPPNVQLTGYRVKVTPKEKTGPMKEINLAPDS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPR	
ARVTDATETTITISWRTKTETITGFOVDAVPANGOTPIORTIR	
DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAF	
NLRFLATTPNSLLVSWQPFRARITGYLIKYEKPGSPPREVVPF	
RPGVFEATITGLRPGTEYTIYVIALKNNQKSEPLIGRKKTDEI	
QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPG	
SGOOPSVGOOMIFERHGFRITTPTTATFIRHRPRPYPPNVGO	
ALSOTTISWAPFODTSEYLISCHPVGTDEEPLQFRVPGTSTSF	
LTGLTRGATYNIIVEALKDQORHKVREEVVTVGNSVNEGLNQF	
DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRC	
SSRWCHDNGVNYKIGEKWDROGENGOMMSCTCLGNGKGEFKCI	
HEATCYDDGKTYHVGEONOKEYLGALCSCTCFGGORGWRCDNC	
RPGGEPSPRGTTGOSYNOYSORYHORTNINVNCPIECFMPLDV	
ADREDSRE	
5364 8066 703 RLCCTGGCBGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLM	VQ
PPSWRRQPPGGIRRDFSRRLRREANLVATCLFVRASLPHRLNN	
RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQNVQPQSPVAV	ИP
	MP IML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptid
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	ocquonoc	*possible nucleotide insertion)
	buquence		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCES
		1	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRI
	ł	1	CTIANECHEGGQSYKIGDTWREPHETGGYMLECVCLGNGKGEW
		1	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWVDCTCLGEGSG
		ì	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGR
	l .	1	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCV
		1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNCVSCQETAVTQTY
	1		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQD
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGR
	l .		DNMKWCGTTQNYDADQKFGFCPMAAHZEICTTNEGVMYRIGDQ
	1		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNV
	1	[DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQ
	1	1	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVF
	l .	i .	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATI
			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTS
	I	1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDI
	i	ĺ	SGFRVEYELSERGDEPQYLVLPSTATSV\NIP\DLLPGRKYIV
			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWS
			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQY
	ľ	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTD
			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AE
		j.	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFV
			ETDSTVLVRWTPPRAQITGYRLTVGLTRRCQPRQYNVGPSVSK
			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPY
		ı	TRVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSI
		!	VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNL
	1		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNCQQGNSLEEV
			HADQSSCIF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPA
	1	ł	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKN
	i	l	GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYECHEST
			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TP
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SW
			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGV
	!	l .	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDN
	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMT
	l		EGLOPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTD
	ļ		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDT
	l		BLQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKF
		1	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDS
) .	ļ.	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIK
			DVRSYTITGLQPGTDYKIYLYTINDNARSSPVVIDASTAIDAP
	1		NLRFLATTPNSLLVSWQPPRARITGYIIXYEKPGSPPREVVPR
	l.	Į.	RPGVTEATITGLEPGTEYTIYVIALKNNQKSHPLIGRKKTDEL
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTCNGIQLPG
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVCQ
	l .		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSA
			LTGLTRGATYNI IVEALKDQQRHKVRBEVVTVGNSVNEGLNQP
- 1			DDSCFDFYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRC
			SSRWCHDMGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCD
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNC
			RPGGEPSPEGTTGQSYNQYSQRYHORTNTNVNCPIECFMPLDV
			ADREDSRE
5365	8066	703	RECCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLW
	1.00		PPSWRRQPPGGIRRDFSRRLRREAMLVATCLPVRASLPHRLNM
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQNVQPQSPVAV
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCES
			PEABETCF)KYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRI
			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEW
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVDCTCLGEGSG

000	18 31		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	
1			S=Serine, T=Threonine, V=Valine,
i i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGKLLQCTCTGNGRG
1	l		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
í		í	
1	J	1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
İ	1	ľ	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	1		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	l .		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1			GDSWEKYVHGVRYCCYCYGRGIGEWHCCPLQTYPSSSGPVEVFI
1	1		
1	1	1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	i	l	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1	[1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	1	I	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1	1	1	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	1		PQAPITGYRIVYSPSVEGSSTELNLPETANSV"LSDLQPGVQYN
1	J.	I	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRJLQFVEVTDV
1		l	KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1		Í	TOT COCUMENTALISM TO A COMMUNICATION OF THE COMMUNI
1	l .)	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	į.		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
J	1	i	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	l		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
		l	HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	ſ	1	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
	l		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
	l	l	
1		1	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1		l.	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1 .			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVTDVODNS
			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1 1	1		BGLQPTVEYVVSVYAQNPSGRSQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1 1			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTA_PAPTDLKFT
1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1			DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1 1	1		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1 1			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
1 1			
1	l l		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
			LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1			HEATCYDDGKTYEVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1 1	1		RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1			ADREDSRB
5366	8066	703	RLCCTGGGBGTPCASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
	55.76	, 53	
1 3	ļ		PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1	J		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQNVQPQSPVAVS
1 1	j		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1			PEARETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1 1	J	1	CTIANRCHEGGGSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1 1		i	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMNVDCTCLGEGSGR
1 1		ļ	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGWLLQCICTGNGRG
1 1			
[]		J	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1 1			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
L			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
.NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KYSPCPDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEBICTTNEGVMYRIGDQW
1		,	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
	1		DTFHKRHBEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1	j		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	1		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	i .	,	PQAPITGYRIVYSPSVEGSSTBLNLPETANSVTLSDLQPGVQYN
			ITIYAVBENQESTPVVIQQETTGTPRSETVPSPRDLQFVEVTDV
			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
I			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTMFLVRYSPVKNE
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1			\LRGRQXTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLINLTPGTEYVV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 .	l		APAVTVRYYRITYGETGGNSPVOEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVIDVODNS
			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
	1		BLQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
			OVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
!			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
J I			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
[RPGVTEATITGLEPGTEYTIYVIALKNNOKSEPLIGRKKTDELP
1			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1 1			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1			ALSOTTISWAPFODTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1 1			LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1 1	1	1	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGORGWRCDNCR
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1 1)	ADREDSRE
5367	235	3591	KKILNMLCKKNIVIBYLADILYEYLYGFCFSGIKKYLIIHVLRL
1		****	ILELWMTRLLLEKSVSLOTOYLLLIVKILSWFPGKEMRHHLOIM
1 1			EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQFGEKELV
1 1			KRSQLDGEGDGPLSNOLSASSTINPVPLVGLOKPEMSLPVKPGO
1 1		1	GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
			SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
1 1		1	LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
			LYSFATAFRRSAKQTPLSATAAPOTPDSDIFTFSVSLEIKEDDG
1 1			KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVOQTTNKELAIERCF
	1		GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
			FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
)			NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLES
1	0.0		ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEERDNDEPLL
1			SGSGDVSKECAEKILETWGELLSKWHLNLHVRPKQLSSLVRNGV
L			PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPCDSAITRDIN

Predicted Predicted Predicted end Incleation Corresponding Corresp				
No: muclectide location corresponding corres	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: muclectide location corresponding corres				(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
corresponding corresponding corresponding corresponding cofirst saino acid cofirst saino acid cofirst saino acid sequence corresponding correspondin	NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first anino acid and acid anino acid acid anino acid anino acid anino acid anino acid anino acid anino acid acid acid acid acid anino acid anino acid acid acid acid acid acid acid acid	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first anino acid anino acid residue of residue of seldue of sel		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of saino acid sequence whyposible nucleotide delation, nucleoti		to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
residue of sequence #HTTPPCOPARM, Y=TYCESINE, X=Unknown, "=Stop sequence #HTTPPCOPARM, Y=TYCESINE, X=Unknown, "=Stop sequence #HTTPPCOPARM, Y=TYCESINE, X=Unknown, "=Stop sequence #HTTPPCOPARM, Y=TYCESINE, X=Unknown, Y=Stop sequence #HTTPPCOPARM, Y=TYCESINE, X=Unknown, Y=Stop sequence ##FPANHIPYENIPOSOPOSITYET (CRAYSYYPSE) 220 CQGQSFIA #Y=TYPANHIPYENIPOSOPOSITYET (CRAYSYYPSE) 220 CQGQSFIA #HTTPPCOPARM, Y=TYCESINE, Y=TYPANHIPYENIPOSOPOSITYET (X=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y=Y	Į.		residue of	S=Serine, T=Threonine V=Valine
amino acid sequence Codon, /-possible nucleotide deletion, Proposible nucleotide intertion) RIFFANDYRUTGHOOGOSTATICKAYSYVPSIGYCGGSFLA AVAILAMBREGARSYNIATHORYCHICARYGUNGSIGAC RIAGATT FOLUNTELDISLAMPYASCAFIT, THAKEPLICYPTE ITOLIACGUI STUTPANIALILITEKULTITEKULTITE				W-Truntonhan V-Turnesine V-Unknown t-Ston
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AVILLIAMPREDAPSVIJKIMPRYGIAELEKENNTEDILICIETYOLE RIMOSYT POI LIVIERIO I SLEAMPINASO PETILITYAKEPI LYVEH 1 TIOLLEGE SIVIERVALGLIATES KUDOLLID PERGALKEPENOUT 1 TIOLEGE SIVIERVALGUE AND THE SIVIERVALGE SIVIERV		sequence		
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1 IIILLEGISTY IRVALGILITER KOLLLITYSKALK PEPUDL. PRYTYSHENAK KHELANNIK 1900 KALKIYKEN YATHROOMOO BDI IRREBERERKI QOANMALOOK KALKIYKEN YATHROOMOO REBERERKI KALKIYA KALKIYA KALKIYA KALKIYA KALKIYA JALKIYA JA	1			AVLLLHMPREQAFSVLVKIMPDYGLRELFKQNFEDLHCKFYQLE
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ED PERFERENRI QUANMILLOTINE LA JARCELO NAMERICADA INVECLIANTIQUE. IN DERERKIR JEESSA HALKOUGH NAMERICADA INVECLIANTIQUE. IN DERERKIR JEESSA HALKOUGH OKTODE CERCE PERFORMING VALUE SERVELVID DED DES PERFORMING NETHER SERVELVIO LA LIBERT VALUE SERVELVE DE DES PERFORMINT SERVEL SERVELVIO LIBERT VALUE SERVELVIO LIBERT VALUE SERVELVIO LIBERT VALUE SERVELVI SERVEL	ł	ł		IIDLLLCEGISVIFNVALGLLKTSKDDLLLTDFEGALKFFRVQL
INABERGALINEGLIATING VILLIDREEKERILEESSAHLIKKOMERSE LIDEASSE ILINGENSI IOT VINCIGESIESKEREOGYANIVETEKIR OKUDCERCREPPINGBRUNGI SERIEMOGYANIVETEKIR OKUDCERCREPPINGBRUNGI SERIEMOGYANIVETEKIR OKUDCERCREPPINGBRUNGI SERIEMOGYANIVETEKIR OKUDCERCREPPINGBRUNGI SERIEMOGYANIVETEKIR OKUDCERCREPPINGBRUNGI SERIEMOGYANIVETYÖN REMERILLARIVETYÖN ÖLÜNDÜR SERIEMOGYANIVETYÖN REMERILLARIVETYÖN ÖLÜNDÜR SERIEMOGYANIVETYÖN ROMAGI TERIT PERSONULOT VINCIGESISKEVINTINGERLEKTYÖVE PHORRILVISLOTUDULUGI KORINPINKTED (LIP-MILARYITIVOTEN MUCCE PEV, GEKKUS PROMINGER SERIEMILLEKTIR YER VINCIGESISKEVINTINGER LEIDINISTY PETRIKUVEL OKUMANIVETYÖN ÖLÜNDÜR SERIEMI ILIKERE ALIFILTISKEVOKLI YERINOV PROMPYPEKEGILEKYÖN VINCIGESISKEVINTINGER VINCIGESISKEVINTI				PKRYRSEBNAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
LDRABSITAMESTIONYGICSGLSERLENGGTANNYETSKIT OKNODICKROEPHORGONYGICSGLSERLENGGTANNYETSKIT STATEMETIASI TENTAVOGRETE TAMBETIASI TENTAVOROGRETE TAMBETIASI TENTAVOROGRETIASI TENTAVOROGRETI TAMBETIASI TENTAVOROGRETIASI TENTAVOROGRETIA TENTAVOROGRETIA TENTAVOROG		l	1	EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
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RTPETPRAGAGPA-SAGGSVYTENSDLTSEASTPSTCRELISSYED ATVES IPENSISVUMLI ISSUMPLEDONSDCC CUCKNOTK GANUSVYTEDPTORAQVECTOGES-AVENAREONSOLFSEDSLD I TIGENTDCGKSERREFREALANDSSKHVOGKSESSKLSBUDLLL LOCCTIPLESPRAADODPFREGVISNWVGERDCCNDCTLA LEBIGGPTOMBOSGVYDEALWESELDHYSERROVSBUGSSDLTL RMLSLQPU-QDATOSKRYTVENWOODPLTWCQTHKWRSGSOTO TDESPREAL PIFFLICHTVIDTLISTPSTAL SPREALPWSERROVSBURSWYSGS DIAYWLCPBIRALINGASSFYRQUTAY INSCRLEGGREPVSELL TOCHHWISTSKERLSEKLNEKMENDFALANTAY INSCRLEGGREPVSELL CKRIGGPTI-ASUPLISSINISTSCALGSTRYVTSKALGTSTS ASSISSIMISSOSSSKKLRSOVSSKKLRSOPPSSINISAAGSSTSVALANSUTTSTSSSSS SINISSOSSSKKLRSPPPERSINISAAGGSSTANTVOGGQLGGG CKTGLGFT-ASUPLISSISSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOGGQLGGG CKTGLGSTSSSSLFOOPPSSINISAAGGSSTANTVOTGGGLGGG				
ATTHE I PERMISLY VINILLISES VINILTED CHISGOCCI CUCHINITIK GARINGVIT I POPULAQVIET CORSENITARY ANTONICE PEDELLI I TORRITO CORRESPONDA CORP. CORRESPONDA				
GANUSVYTEDPTORAQYBETCGGESAVROTAREONISOLIFEDEBLD I TIGRIPTOGAGAREARFERALARIJAS ERWIONGLKESSKLEDILLL LOCCTIPLESPRAADOD PPREGVISNIVVERROCKINCTILL LEBEGROPHINBENGSKUVERLIVESKLEDVSKROVSKORGSOD II RMLSLQPVLODATOSKRYVERNOVODPLIVKOCTHENDSKOSOTO TOESPBEBLEPTFLICHTOTHILLY PREAPTAPHENEL HANDEVSOR DIAYVVLCPBIRLAINMANSFYRUTAT Y RESCLEGGBRPVSELL TOCHHAVIGTSKELGERLANDEVSAACHSKELSEKLEKLANDV CRYDIGPTLASUP, DISSLIGOPBLIVATSTOSLITPPOMITTONA MTPSATLASARSPHYVITSKYA JEVALARISTICTSESSS SINLASOVSSKIKLBEPPERSINSKAAOSHSTOANTVOGOLGOG GYSALOZAGISASSKLOPPEPPSSNISKAAOSHSTOANTVOGOLGOG GYSALOZAGISASSSKLOPPEPPSSNISKAAOSHSTOANTVOGOLGOG GYSALOZAGISASSSKLOPPEPPSSNISKAAOSHSTOANTVOGOLGOG GYSALOZAGISASSSKLOPPEPPSSNISKAAOSHSTOTOGOSK	1			
I TORNYDCOKEARRYPHANIS REHTWOGLKSSEKLSDDLILL LOCOCTHLESPERADOOP PERSON INNIVERSERCONNOCIA- LEHGROPHINNEGGKVOBALVESCLEPPSERTOVSN(CSQD LL HMLSLQPVLODA DOKKRYPHENDOOPD-INCOCHTRONISGISTO THESPERI-PIPTILIOTYDTININEPRALPYRE MALEPYGSQF DIAVYNLOPBERILI MORASY PRINTINIT I SECHLÖGGEV VSEILL CONTIGENTAL OF THE STANDARD OF THE S				
LODOCTHLASPROADOD PPPRISOTI SINVAYUERDOCKINCYLA LEHERGOPHINERGOS VUDBALIVESCLEH PERENTVORINGCOSO I I RMLSLQPULODATOSKRYTVENWOOD PLIVOCYTHUNGKSSTO I DESPREADE PPPLIADYIDYITULA USPPRALIPAREN LANDERSOGO DIAYVUCPERRALIMARSPYROUTAT YRSCHLOGREPVESLIL TICHIRVISTRAKELBERIMARPOOLAGORIAPROSE PRISOTION CREDIGFILASUPLISSILSOPRILVASTOS GILTPPOPHITYONA MYPSATLASARSPYTVISTOKAT JESVALANSILTISTESS SS SIMLASOVSSIKLIDEPPERSINSIAAGOSETJOANYTVOGOLOGO OTSALOZAGIS SESSESENDYDESVASTINDESTOKATIVTOGOLOGO OTSALOZAGIS SESSESSENDYDESVASTINDESTOKATIVTOGOLOGO OTSALOZAGIS SESSESSENDYDESVASTINDESTOKATIVTOGOLOGO OTSALOZAGIS SESSESSENDYDESVASTINDESTOKATIVTOGOLOGO	0.0			
LEHERGOPHINN-SGGKVIDBALVESGCLEPPSERFOVENGCSGO ILI HMILSLOPULOGLO KORKTVENDENO OPDITACOFTENGRISGIYO TDESPERLEPTELLOPYDYILILEPPALPYBELALEPPVSGGE DIAVVILOPBERLAHINNERSPYSHILAT YESCHLOGEPVSELL TOXINN-VISITAGERLOERINABURYSHILAT YESCHLOGEPVSELL TOXINN-VISITAGERLOERINABURYSHOLATOSHIAFPVSGLAL TOXINN-VISITAGERLOERINABURYSHOLATOSHIAFPVSGLALIJAGOV HTPSATLASAASSHTVYJTGOVI, ATSVANDASILITAGESSESS SHLINSOVSSIKLIDEPPPSGNINSINAGORSTOANTVQGQLAGO GYSALOTAGISSSSSLOTOGROPPVSTRYDENTSTYTOGENST	1			
RMLSLQPVLODATOKRYTYRPHOYOOPITMOCPHEMORGSTO'D TDESPBEBLEPTFLICHTOPITLICHEPTSPLAPMERISHENBYPSOGN DIAYVVLCPBIREALINGRASFYROLTA'I YSECHLOGISRPVSELL TOCHHAVIGTSREKLISEKIALSRYPADALORINER,PEKLIKLIVAOV CRYDIGPTLASUPLISSLIS.OPINLIVATSTOSLITPPCHITTORN MTPSATLASASSPHYVTSTOYA I STVATANSILTITATSTSSSS SINLASOVSSKIKLBEPPPESSINSRAAGOSHTOANTVOGOLGOG OTSALOZAGISRSSSLFOOPPPUSSTNORENVESTORATVETTOFGESS				
TDESPERLP IPTF, IACYDYNYLIALSPRA, DYWERLALBPYGSOR, DIAYVILCEBURAL MINGASY PRINTAT Y RECHLIGAPPUSELL TDEIMRYUSTASKKILSEKINASWYSPRAITAT Y RECHLIGAPPUSELL TDEIMRYUSTASKKILSEKINASWYSTASKAIST TYPOOTHYTORA MYTERATLASASSYTYVISTORY AISY VALANSILTITETSISSES SMANOVSSKKLDSIPPERSHNINAGOSHITOKHTYCOGLIGOG OTSALOZAGISTASSESSLPOPEPENSYSTYMORIVETTOLOSKI				
DIAYVUCPBREALINGASSPYRUTAT IRSCHLÖGBRPVSKLI. TUDIHRWIGTBAKKLISERINABPOJAAORINEA PEKULTAJOV CRYDLÖFTLASUPLISSILSOPRILVASTOSOLITPPOMITYGAN. MTPSATLASASSPHYUTUSVAJ ISTVALVASILTJASTSSSS SINIASOVSSKKLÖPPPPSSNISNAAOSHSTOJANTVOSOLLOGO OTSALOTAJOSSSSLÖPPPSNISNAAOSHSTOJANTVOSOLLOGO OTSALOTAJOSSSSSLÖPPPSNISNAAOSHSTOJANTVOSOLLOGO OTSALOTAJOSSSSSLÖPPSPSNISNAAOSHSTOJANTVOSOLLOGO				
TUJIHKYUSTRAEKILSKUJASWFSQAAJSMRAFSKLIKIJAQV CKYDLOPVIASUPIJESLLSQPHIJAPTSQSLITPSQUSTUPOUTTORN. NTPSATLARJASSTHYVISGVAJISTSVITANSTLITTASTSSSS SMLASOVSSKKLDSPPPSSNSNAAGOSSTÇANTVQGQLGOQ (GYSALGAGISTSSSSLIVOPSPYSSTMOKEKVST PTOLOSH				
CRYDIGPTIASUPINSULSGOBALWARTSGOLTPPOWITTONA MTPSATLARASSIPTUTSGOAT, SIX VALANSILTIPATSESSS SIMANGVSSIKU, DEP PPERSIMSINAGONSTRANTYCGOLLOGO GTSALGZAGISESSSLOTOPEP DVSSTYMGERWYST PTOLOSH	1			DIAYVVLCPENEALLINGAKSFFRDLTAIYESCRLGQHRPVSRLL
CRYDIGPTIASUPINSULSGOBALWAFTSGOLTFPOWITTGAN. MTPSATLASASSIPTUTSGOAT, SISVATANSILTIFATSESSS SIMANGVSSIKLIGSFPPERSIMSINAGGHSTGANTYGOGLGOG GYSALGZAGTSGASSSLFOOPPDFUSSTMORDWSTFOODSH				TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAOV
ntbratlararstytungva istsvatansiltilasissis snlnsgvssnklprpppgsnnsnaagsstyanivogolog gysalgyratssesslptophedvsrthorevsiptdedsh	 			
SNLNSGVSSNKLPSFPPFGSMNSNAAGSNSTQANTVQSGQLGGQ QTSALQTAGISGBSSSLPTQPHPDVSBSTMDRDKVGIPTDGDSH		1		
QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH				
	X-			
THE THE THE PROPERTY OF THE PR				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	sequence	
	sequence		\=possible nucleotide insertion)
1			TLPPHIKSTVSVQIIPCQYLLQPVKHBDREIYPQHLKSLAFSAF
			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
1	ľ	1	FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
1		1 2	TDLYGELLETCI INIDVPNRARRKKSSARKFGLQKLWEWCLGLV
1			QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
i	Į.	l	CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
	l	1	TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1		l	AFNPNNDGADGMGIFDLLDT3DDLDPJIINILPASPTGSPVHSP
1			GSHYPH3GDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST
1			AKAGPLPDWFWSACPOACYCCPLFLKASLHLHVPSVOSDELLHS
1	1		
ì		l	KHSHPLDSNQTSJVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
			FVVLNQLYNFIMNML
5370	1226	716	RWSRKLBLRRAAQATESRPPQSQEMHPFTGKEVHALKRLRDSAN
1	l		ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
1		1	DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
1			AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
1			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
ì		ļ	AVRPLSSAAOGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
1	l .	Į.	GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
3372	2332		SKENTRIVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
1			LQBLGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
1		ł	ELIKLIEGFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
1			AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSO
			NPFILLNSPTAIKETLEFLQEGGFTSFEILQLLSKLKGFLFQLC
1	i	(PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
			QGLLREGISIAQIRETPMVLELTPQIVÇYRIRKLNSSGYRIKDG
1	1	ļ	HLANLNGSKKEFSANFGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFIWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
33/2	31	057	
1			PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
1	1	ŀ	RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
ì			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
1			HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
1		ŀ	SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
	L		KTGÖG
5373	2814	346	VKKTKSIFNSAMQEMBVYVENIRRKFGVFNYSPFRTPYTPNSQY
1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1		1	TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1		ľ	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
(l	KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1			IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
1	i	1	DSSDSEYISDDRQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
1		l	TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
1	i .	i	PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
1			GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
1	1		TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
1		l	
1			AVQRSCGTSSTVQQKETTQSPSTSTITLVTSTQSSPLVTSSGSM
1		1	STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
1			YNDLSKM\TTWKAQLAEDSQGLRIBIEKLQWLHQQEL\SEMKHN
1		i	LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
1	1		ANFKKBAIFYCCWNTSYCDYPCO\QAHWPEH\MKSCTQSATAPQ
1			\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
1			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
1	1	1	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESKAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1	1		TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1	1		ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1		l	KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1			IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
1	1		DSSDSEYISDDEOKS*GTSOEDTEDKEGCOMDKEPSAVKKKPKP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TNPVEIKERLKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
			PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
		1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
			AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
İ	i	Ĭ	STLVSSVNGDLFIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
			YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
			LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
			ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
			\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
1			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIPLAREEPMLERECEGPLAMGPAQPELLSGPSQESPQTLGKES
			RGLRQQGTSVA\QSGAQAFGRAHRCAHCRRHFFGWVA\LWLHTR
ļ			RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
'		1	SSILRRCHPSRPRGPRPFICGNCGRSILPTWDO/LKVAHKRVHV
			SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA
			CCGKRFRHK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY
		1	LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
			AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
			QDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC
		1	GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN
			SABPNAPRFGPFVCPDCGKAPRHKPYLAAHRPIATPAEKPYVCP
			DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNYAQSKRHVYSRTPSGSRMSAEAS
33/6	4504	291	ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKNVGVILDEAKG
1	}	1	KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
		l	SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
			ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP
		1	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
	1	ì	KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL
	}	1	BAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER
		l	VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEEQNARLKDALV
			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVEQQRERLQEELSQ ABSTIDELKEQVDAALGAEEMVEMLTDRNLNLREKVRELRETVG
			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ ARSTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETUG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA
			RMRDLSSSEKGEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ ABSTIDBLKEQVDAALGAEEHVENLTDRNLNLEEKVRELEETUG DLEAMNEMNDELQENARETEELELREQLDMAGARVREAQKRVEAA QBTVADVQQTIKKYRQLTAH:QDVNRELTNQQEASVERQQQPPP
			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ ARSTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETUG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA
			MMRDLSSSKOEHVA\LOKIMEKKNOKLEVVRQORBRICEBLSG ABSTIDELKEQVDAALGAEHVEMITDRNINLREKVRELRETVG DLEMMENNDELGENARETELEILEGGLDVAGARVREAGKRYEA GETVADYQGTIKKYRGLYAHL-QDVINELINQGEASVERQQQPPP ETFDFXIKFAETKALAKA LEHELKOMEVAQARRHMSLITAFMPD
			IMBOLSSSENGERVY. LOGILMEKKUSOLLSVYROOPERILGELSG ABSTIDEKKESODALGABENVERTURFANLESEVELERVO DLEAMINSHIDELGENARETELEKEROLDSVARARVERACKEVERA OETVADVOGTISKTELGLARIOLDSVARARVERACKEVERA OETVADVOGTISKTELGLARIOLDSVARARVERACKEVERA SERREGORDIOVILLIAMPALICHERLIKKOAGERETISHCOS FROGLERAAGKOLSFRATOLDVY, SLUPRACHEVIREY CERLISCOS REGLERAAGKOLSFRATOLDVY, SLUPRACHEVIREY CERLISCOS LOVVKKVASJATUREMARKESJATILLHLENDLESTVARELT
			RMEDLESSERGENTK LOGILMERCHOGELSVYROCKERICELSG ABSTIDERLEGODALGGEBEUWSCHIDTENLINEERVERLERTVO DLEAMINENDELGENARGETELEREGOLDWGARVERACHVERA GETVADVOGITEKTELTALGAK I EMELIKARISHVAGARREGOLDFER ETTOPELIKARITALGAK I EMELIKARISHVAGARREGOLDFER ETTOPELIKARITALGAK I EMELIKARISHVAGARREGOLDFER ETTOPELIKARITALGAK I EMELIKARISHVAGARREGOLDFER ETTOPELIKARITALGAK I EMELIKARISHVAGARREGOLDFER ETTOPELIKARISHVAGARREGOLDFER ENGLEGARGIOGERATALIVY SEPANGHYRITET VILHAGOR ENGLEKARIGOLDFATALIVY SEJANDHYRITET VILHAGOR ENGLEKVAGINUS GERMANISH SLOPIJ ELLHROGIDETVAVEDLI KARKYVGHIN SELIKAROPENTAMIN SHIFT KARGARDOLOKUSVU
			IMMOLSSSENGHTV. LOGILMEKKUSOLLSVYROOPERILGELSO ASTITORIKADVAALGABENVENTUDERIMLISEKYPELERTVÖ DLEMMISHNDELOGNARFIELERSÖLDHARAVERROKTYBAA ÖRTVADYOGI TEKKRÖLTAHLOGNARFIELTOGASPERGORFPE ETFDFK KRAFTKAHAKA EMEKRANEVAJARAMISHLINGASAPERGORFPE SFLROGGIDUVULLIMPRELLOKELIT KRAGARFIELSENGES ROGLERAAGSGLSFAATOLIVY SLUPAAGHRYTEY "CHALSOCK ROGLERAAGSGLSFAATOLIVY SLUPAAGHRYTEY" CHALSOCK KALKYVOLLVS LIILBAGDEBOCTMOLADHIKTOGALDCHSVEN KALKYOLL LIILBAGDEBOCTMOLADHIKTOGALTHON KALKYOLL LIILBAGDEBOCTMOLADHIKTOGALTHON KALKYOLL LIILBAGDEBOCTMOLADHIKTOGALTHON KALKYOLL LIILBAGDEBOCTMOLADHIKTOGALTHON KALKYOLL LIILBAGDEBOCTMOLADHIKTOGALTHON
			RMEDLESSENCHTK LOGILMEKKUNGGLEVYNGORERUGGELSG ABSTIDERIKGOVALAGABEWYRITDERFAILESEVYNGORERUGELSG DLEAMISHNDELGENAGSFELEKREGLDDAGARVERAGRYFRA GETVADYOGI TEKTRELTERIGDASVAGRAVERAGRYFRA ESTADFORD EVYNELLYGGLESSENGORYAGARVERAGRYFRA SERREGGENEVYLLAGRELIGERUGENGORYAGARRINGLUTAFRED ESTADFORD EVYNLLAGRELIGERUGENGORYAGARRINGLUTAFRED ESTADFORD EVYNLLAGRELIGERUGENGORYAGARRINGLUTAFRED LOVYKKNOSLYFENGARRES SLEPLI ELLEGOLDETYNGELT LOVYKKNOSLYFENGARRES SLEPLI ELLEGOLDETYNGELT ARITYYOLING ELLEGABERT ENDER ENDE
			IMBOLSSSENGHTV. LOGILMEKKUSOLLSVYROOPERILGELSO ABSTIDKIKSOVAALGABENVENDIDENIMISE SYNDOSHELETVO DLEMMISHNDELOGNARSTELEKROOLDWARRVERACKIVPAA OETVADVYOJI TIKKROLTAHLOOMISLINGOBASVERACKIVPAA SETVADVYOJI TIKKROLTAHLOOMISLINGOBASVERGOOPPP ETEPSKIKRATKALKAKA LEMEKROMEVAJANEMISLINAPREP SELREGOBIOVULLILMERILGKELEKROMEVAJANEMISLINAPREP SELREGOBIOVULLILMERILGKELEKROMEVAJANEMISLINAPREP ROGILGRAGISUSPAATOLIVY SLUPAADHRYNEY "CHALSOCK ROGILGRAGISUSPAATOLIVY SLUPAADHRYNEY" CHALSOCK REARPLOGOSTOTI TILLILABOLDERIS OLIGIPOKUK SIRRINOT DAPSI PAALAFROJOSIULTULGKIKULTUVVALGKVAAAAAQLI ARJARNISLAALAEELEKRASSOTI TYOTPSSSY PECKAGSCITI.
			IMBOLSSSENGENTY LOGILMEKKUNGGLEVYRGORERUGELSG. ABSTIDELKSODALAGABEWYRTDTRYMLESENYBLERTVO DLEAMISHNDELGENAGSTELEKREGLDWAGAFVERAGRYERA GETVADYOGI TEKTRÖLTHLEGORITORLINGESENGGOPP ETFPS LIFABTKAHARA EHEELROBVAGANARMSLUTAFVER ESTARGGORITOVILLIAMPELLOTALELINGAGARFYERAGARFYERA ERGILKAGAGGLEPRATOLIVY (SLIPAAGHRHYNY CERLISGOS ERGILKAGAGGLEPRATOLIVY (SLIPAAGHRHYNY CERLISGOS ERGILKAGAGGLEPRATOLIVY (SLIPAAGHRHYNY CERLISGOS ERGILKAGAGGLEPRATOLIVY (SLIPAAGHRHYNY CERLISGOS ERGILKAGGENTOLILLEDLETEGS) DIDDCKKLIRENDOT ERBAFLGGOGRATOLILLEDLETEGS) DIDDCKKLIRENDOT ERBAFLGGOGRATOLILLEDLETEGS) DIDDCKKLIRENDOT ERBAFLGGOGRATOLILLEDLETEGS) DIDDCKKLIRENDOT ERBAFLGGOGRATOLILLEDLETEGS) DIDDCKKLIRENDOT ERBAFLGGOGRATOLILEDLETEGS) DISDCKKLIRENDOT ERBAFLGGOGRATOLILEDLETEGS) DISDCKKLIRENDOT ERBAFLGGOGRATOLILEDLETEGS) DISDCKKLIRENDOT ERBAFLGGOGRATOLILEDLETEGS DISDCKKLIRENDOT ERBAFLGGOGRATOLILEDLETEGS DISDCKALIRENDOT ERBAFLGGOGRATOLICENDOT ERBAFLG
			IMBOLSSSENGHTV. LOGILMEKCHOOLISVINGORERIGGELSG ABSTIDEKKENDALAGBENVENDITDERMILSERVINGORERIGGELSG DLEAMISHNDELOGNARGFELEKRIGOLDWARRVERGENGENGEN GETVADVOGTISKTELGERSGOLDWARRVERGORYERA GETVADVOGTISKTELGERSGOLDWARRWELLTAFRED ETFDFKIKFAFTKAHAKA EMEKENGENGANARRWELLTAFRED SELREGGEIDEVULLLIMFRELLGERLEITKGAGERFELSEIGES RFGLEGAAGSGLISFAATGLIVY, SLEPHADRHYRTY-CHALSOCK RFGLEGAAGSGLISFAATGLIVY, SLEPHADRHYRTY-CHALSOCK REARFLOGGORTDI-BLILHERGDETWAVELIT KAIKYYGELINSILIHABGDEBCTWILDLIHREDGLETWAVELIT AGARTYGELINGTHIALIBAGESCON JERGPCKKINGSCHIL JASHIGHLANALEELAFKASGLYTTOTSSSEYFECKGSCHIL ISTNINK, LVTANGGSETDARRPPSKPPPVVERLARALIKARSITDA BGLGLALLBERFUN KEKLESKIK JEESELSEANVILLERKIDS
			IMBOLSSSENGENTY LOGILMEKKUNGGLEVYRGORERUGELIGG ABSTIDELKGODALIGGEBUNGGUTUDFALMEEKTYRGORERUGELIGG DLEAMISHNDELGGNAGSTELEKRIGDDAGARVERGGRYEAA GETVADYGGT IKKREITLEKRIGDADAGARVERGGRYEAA GETVADYGGT IKKREITLEKRIGGNEVAGARVERGGENEYAA SERREGGBIOVULLIAMFRIL LYGGLEBELTRAGARVERGGENEYAA HOLVYKKYSELTENSAGRKESTELTELLEKRIGGESTELSBRICGS REGILEGGAGGGLEFAATGUTVÄLSERBAGHKETTÄTTÖRÄLTIGGAGGT KALVYKKYSELTENSAGRKESTELTELLEKRIGGESTENSE KOLLEGGAGGGLEFAATGUTVÄLSERBAGHKETTÄNGAGGT ABAGT BAALBAGFTAGAGGT ABAGT BAALBAGFTAGAGGT ABAGT BAALBAGFTAGAGGT TISTNIK'LVATAGAGGT ABAGT BAALBAGFTAGAGGT TISTNIK'LVATAGAGGT ABAGT BAALBAGFT BAGT BAALBAGT BAGT
			IMBOLSSSENGHTV. LOGILMEKCHOOLISVINGORERIGGELSG ABSTIDEKKENDALAGBENVENDITDERMILSERVINGORERIGGELSG DLEAMISHNDELOGNARGFELEKRIGOLDWARRVERGENGENGEN GETVADVOGTISKTELGERSGOLDWARRVERGORYERA GETVADVOGTISKTELGERSGOLDWARRWELLTAFRED ETFDFKIKFAFTKAHAKA EMEKENGENGANARRWELLTAFRED SELREGGEIDEVULLLIMFRELLGERLEITKGAGERFELSEIGES RFGLEGAAGSGLISFAATGLIVY, SLEPHADRHYRTY-CHALSOCK RFGLEGAAGSGLISFAATGLIVY, SLEPHADRHYRTY-CHALSOCK REARFLOGGORTDI-BLILHERGDETWAVELIT KAIKYYGELINSILIHABGDEBCTWILDLIHREDGLETWAVELIT AGARTYGELINGTHIALIBAGESCON JERGPCKKINGSCHIL JASHIGHLANALEELAFKASGLYTTOTSSSEYFECKGSCHIL ISTNINK, LVTANGGSETDARRPPSKPPPVVERLARALIKARSITDA BGLGLALLBERFUN KEKLESKIK JEESELSEANVILLERKIDS
			IMBOLSSSENGENTA LOGILMEKKUNGGLEVYNGORERIGGELSG ARSTIDERIKGOVALAGABEWUNGDTENTMIESERYNGORERIGGELSG DERAMISHENDELGENARGEREELERFOG DERAMISHENDELGENARGEREELERFOGLDWAGARVERAGREVERA GETVADVOGOT IKKTROLTANI-GOWERLENGGORPPE ETPDYE IKRAETKACHAK LEMELKONEVAGURENSELLDAFFED ETPDYE IKRAETKACHAK LEMELKONEVAGURENSELLDAFFED ETDYE IKRAETKACHAK LEMELKONEVAGURENSELLDAFFED ETDYE IKRAETKACHAK LEMELKONEVAGURENSELLDAFFED ETDJEGAGMANGUSPAATALIAV SIE HARDISHYTEN ET GLAGGER LDVYKKVSISLYEMSARATIAV SIE HARDISHYTEN ET GLAGGER RIKAFYGGORATDIALIKEDLETGGS DIERPOKKKI RIKBINDT RIKAFYGGORATDIALIKEDLETGGS DIERPOKKKI RIKBINDT RIKAFYGGORATDIALIKEDLETGGS DIERPOKKI RIKBINDT RIKAFYGGORATDIALIKEDLETGGS DIERPOKKI RIKBINDT RIKAFYGGORATDIALIKEDLETGGS DIERPOKKI RIKBINDT RIKAFYGGORATDIALIKEDLETGGS DIERWAGHLIKENLING RIKBINDELLVAALEELAFFASTGI TOTT SISSEY FECTAGGCSTIL RIKBINDELLVAALEELAFFASTGI TOTT SISSEY FECTAGGGSTIL FERGUR FETAGGI TOTT SISSEY FETATT SISSEY FETAGGGOT SISSEY FETATT SISSEY FETATT SISSEY FETATT S
			IMBOLISSISRICHIYA LOGILMISKINGOLISVYROQUBERLOGELISO ASTITORIKA ODDALIGABEWARIDENIMAS ERVIROQUBERLOTUG DLEAMISHNDELOGENARSTELERROGIDMAGARVEROCRIVERA DELEMISHNOELOGENARSTELERROGIDMAGARVEROCRIVERA GETVADYOQI TEKROLITARIOQUBERLOGUBERQOPPP ETPPEK IKPARTKALIKAL EHEBERGIBVAGARRIMSILTARIPRO SERROGIDMOVILLIMARELICERBERGIBVAGARRIMSILTARIPRO BERGROGIDMOVILLIMARELICERBERGIBVAGARRIMSILTARIPRO BERGROGIDMOVILLIMARIMI DELIMINARIPRO BERGROGIDMOVILLIMARIMI DELIMINARIPRO BERGROGIBVAGARRIMI DELIMINARIPRO BERGROGIDMOVILLIMARIMI DELIMINARIPRO BERGROGIBVONI BERGROGIBVAGARRIMI DELIMINARIPRO BERGROGIBVAGARRIMI DELIMINARIPRO BERGRADI PERKESOLILIMARI BERGROGIBVONI
			IMBOLSSISKIGSTYK LOGILMEKKINGGLEVYRGORERIGGELSG ABSTIDERIKGOVALGABEAVERTUTERVILLEERVYRGORERIGGELSG DLEAMISHNDELGGENAGETELERREGLDDWAGAVERAGREVERA GETVADYGGI TEKTRELTERIGGDSWAGAVERAGREVERA GETVADYGGI TEKTRELTERIGGENSVAGAVERBOLDTAFFED ETYDFI KEPATTALERAK LEMELROGIOVAGAVERBOLDTAFFED ETYDFI KEPATTALERAK LEMELROGIOVAGAVERBOLDTAFFED ETYDFI KEPATTALERAK LEMELROGIOVAGAVERBOLDTAFFED ETYDFI KEPATTALERAK LEMELROGIOVAGAVERBOLDTAFFED LADVYKWASLIVELARGE GETOTALERIK GAGGETTAVELE LADVYKWASLIVELARGE GETOTALERIK GAGGETTAVELE RAKTYYGHUN ELHABOP GETOTALERIK WYAVALGENARAAGLI APLARIBELLIVALEELAFASED TYOTE SSSYYECLAGGETTI STENNIK TUNTALERIK KERELE BENVILITLEREKLÖS ANGARDINER INKOVILLERIK KERELE BENVILITLEREKLÖS ANGARDINER INKOVILLERIK KERELE BENVILITLEREKLÖS GALPOGAGSVAGSTERFI GAGGETTARER FERSTEN FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETTARER FERSTEN FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GALPOGAGSVAGSTERFI GAGGETERFI FALTOMAGIN TOL GAGGETERFI THAVITATIS TOLDES FALTOMAGIN TOLLERI TOLLER LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES FALTOMAGIN TOLLER LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES FALTOMAGIN TOLLER LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES FALTOMAGIN TOLLER LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES FALTOMAGIN TOLLER LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES TATUR TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FALTOMAGIN TOLDES LANGSVAGSTERFI THAVITATIS FAL
			IMBOLSSSENGSHYK LOGILMEKKUNGGLSVYNGORERUGELSG. ASSTIDELKGYDDALGGASELWYNDTDWALLGES KYPELERTVO DLEAMISHENDELGDNALGGES LYGDDALGGASELWYNDELLDRYNG GETVADYOGI TEKKELGLYAS. GETVADYOGI TEKKELGLYAS. GETVADYOGI TEKKELGLYAS. GETVADYOGI TEKKELGLYAS. GETVADYOGI TEKKELGLYAS. FELDROGOROUTUHLALMEBLICKERLIKUNGABERELSERGSE BELREAGANGSUSPADILTVY LABHAGHERYST VERLEGGES LDVYKKVSSLYPENSABRESIDPJLELLHENGLDSTVAVEELT ARKYVGINLYAS. FELDROGOROUTUHLALMEDLSTCSS (DIRPOPCKKISRENDOT ARKYVGINLYAS. FELDROGOROUTUHLALMEDLSTCSS) DIRPOPCKKISRENDOT ARKYVGINLYAS. GENERALSENDELSTVANIAGENTANAGLI TISTNIN (LYTANGGSSTDABEPSRFPPVILELHARALIAGRITTA ARKADIKKINGABERTY KERLESKIK KERSESFETMINIAGANITA ARKADIKKINGABERTY KERLESKIK KERSESFETMINIAGANITA ARKADIKKINGABERT BERGALIKKERSESFETMINIAGANITA ARKADIKKINGABERT BERGALIKKERSESFETMINIAGANITA ARKADIKKINGABERT BERGALIKKERSESFETMINIAGANITA ARKADIKKINGABERT BERGALIKKERSESFETMINIAGANITA ARKADIKKINGABERT BERGALIKKERSESFETMINIAGANITA ARKADIK PURPAKANITANI
5377	762	1106	IMBOLSSISKIGHTY LOGILMEKKINGGLEVYRGORERIGELIG. ABSTIDRIKGOVALIGGELWYRDORLOGRUNGGREGELIG. DLEAMISHNDELIGENOGETELERROGLDWAGARVERAGRYERA BETURANGOVALIGAEWYRDIALOGRUNGHUNGLAWGROGYPRA BETURANGOVALIGAEWYRDIALOGRUNGHUNGLAWGROGYPRA BETURANGOVALIGAEWYRDIALOGRUNGHUNGLUNGLUNGHUNGLUNGHUNGLUNGHUNGLUNGLUNGHUNGLUNGHUNGLUNGLUNGHUNGLUNGHUNGLUNGLUNGHUNGLÜBT.
5377	762	1106	IMBOLISSISKOSHYK LOGILMEKKINGOLISVYROORBERLOELISO ARSTIDELKEVODALIOGASEAVENTUDERALINES EVYTOORBERLOELISO DLEAMISHENDELOGNAGERELEELROOLDMAGARVERACKINSPALLETVO DLEAMISHENDELOGNAGERELEELROOLDMAGARVERACKINSPAL EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOOLDMAGARVERACKINGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVALKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILKYVOOLINGERASSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINTIINTIINTIINTIINTIINTIINTIINTII
			IMBOLSSSENGENTX LOGILMEKKUSGOLSVYROGORERUGELISG ABSTIDELKSODALGGABEWSENTDERNINGESTVORGORERUGELISG DLEAMISHNDELGGALGABEWSENTDERNINGESTVERLERTVG DLEAMISHNDELGGALGABEWSENTELEKREGLDDAGARVERAGEVERA GETVADYOGI TEKTRÖLTSHLEGGALGAGURERUGENGAGURERE EFFDELKERSTKAHARA EHBELRINGBVAGARRHÖSELTAFFEDD EFFDELKERSTKAHARA EHBELRINGBVAGARRHÖSELTAFFEDD EFFDELKERSTKAHARA EHBELRINGBVAGARRHÖSELTAFFEDD EFGLERGABGURFRALIDITY (SLIPRAGHERHY)* CERLISGGCS EFGLERGABGURFRALIDITY (SLIPRAGHERHY)* CERLISGGCS EFGLERGABGURFRALIDITY (SLIPRAGHERY)* CERLISGGCST ERRENGAGGCSTANDELLIEDHETTEGS DUTBOCKSTERRENGT ERRENGAGGGTSTARSPERSPEP VERLIAGGCSTL ESTENRY (LUTRAGHER) ENGENDELTVORTAGARGURFRALIDITAFSTENDELTVIRLERGENGS ENGENTELTVIRLERGESTENDELTVIRLERGENGS ENGENTELTVIRLERGENGSTARSPERSPEP VERLIAGARITOTA BOLGLERGHERGSGKTARSPERSPEP VERLIAGARITOTA ENGENTELTVIRLERGENGSTARSPERSPETTENDAGATIOTA ARKARELGRIBAGSGKTER EDILGGEPS SCHATT VSSTAGSEGGR ARKARDHARI ERROGGELVERSHLAGGSTARSPERSPETTENDAGATIOTA ENGENTELTVIRLERGENGSTARSPERSPETTENDAGATIOTA ENGENTELTVIRLERGENGSTARSPERSPETTENDAGATIOTA ENGENTELTVIRLERGENGSTARSPERSPETTENDAGATIOTALSTENDAGATIOTALSPETTENDAGAT
5377	762 2009	1106	IMBOLISSISKOSHYK LOGILMEKKINGOLISVYROORBERLOELISO ARSTIDELKEVODALIOGASEAVENTUDERALINES EVYTOORBERLOELISO DLEAMISHENDELOGNAGERELEELROOLDMAGARVERACKINSPALLETVO DLEAMISHENDELOGNAGERELEELROOLDMAGARVERACKINSPAL EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOOLDMAGARVERACKINGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVYTOORBERLOONAL BEREIKRINGEVANGERISSELLISTRIPOP EVALKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILKYVOOLINGERAANINGEVANGERISSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILKYVOOLINGERASSELLISTRIPOP EKILKYVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELLISTRIPOP EKILTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINVOOLINGERISSELTIINTIINTIINTIINTIINTIINTIINTIINTIINTII

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B*
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Nethionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		
[residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	 		SFSFRNSKQTYSGVPIIAANMDTVGTFKMAKVLCKS*VPGSFWD
1	1	1	VPOMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
		!	
1		ļ.	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
1	ł	1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
		t	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
í	1	i	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
1	1	Į.	BLIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1		i	
1	1	I	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
1	J	1	VNPIFSEAC
5379	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
	1	ł	RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
	1		SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
1	1	1	VPQMGCVPLIYKLFTLKWKKLLLSVLLPASILVAEKFSLFTAVH
į.	I	1	
1	l	1	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
1	I	1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
i	I	1	BELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
1	I	1	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
l .	1	1	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
		1	
1	1		PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
			VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
1	1	i	SQPSSNRAAPQDELGGRGSSSSSSSQKPCEALRGLSSLSIHLGME
1	1		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
í	í		SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
!	1		RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1	l .		
1	i		YNBNDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
	l .		RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
(F\BLVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1	1	1	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1		ł	FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
i	l .		
J	I	J	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1		1	KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
1	ł		ILVKTMIRKRSFGNPFEGSRRBERSLSAPGNLLTKKPTRECESL
1		l .	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
	l .	1	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
	l,	Į	PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGARGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
2207	2	050	
1	}	1	SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1	1	I	SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1	1		SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1	1	I	RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1	1	(YNENDNTYYAMKVLSKKKLIROAAFPRRPPPRGTRPAPGGCIOP
1	1	I	
1	1	l	RGPI/EQVYQRIA/ILKKLDHPNVV/KLVEVL/DDPNEDHLYMV
1	i	l	F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1	1	l	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
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Į.	1	l	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
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1	l		RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
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ı	1		RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
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LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLCAAWVADGVQCDRTVVNGIIATVVVSWIIIAA		1		
ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1 1	i		
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SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(AwAlanine, CwCysteine, DwAspartic Acid, E-
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H-Histidine, I=Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
			IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
1	i	1	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
1			VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
		1	T DUD STOCKED TO THE TOTAL OF THE PROPERTY OF
í	i		LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
1			KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
			ALLATWVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
1			KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
			GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
1			DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1			FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAOGVSSV
1	1	l	DVA
5388	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACOARRPAARS
1		1	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1			TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPRAQSALDST
l .	1	1	SSSNQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	1		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
			TVVYTVTOMYTIALTITKONLKNFVFOOEFKSFGSFHOOLLEYK
5389		753	ILEHLQTKN
5389	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS
	i .	i	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
	i	ľ	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
	I		SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	į.		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
	1	ſ	TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
!		ł	ILEHLQTKN
5390	217	1332	ROPRKLMEDKMWSKCEGPEMSLVCLTDFOAHAREOLSKSTRDFI
			EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIOGERI
	i	ì	SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
ļ	I	ļ	LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
Į.			
	1		LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
[I		ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
			LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEKAPGTVMERRLGVRAWVKENRGSF
I			QPPVCNKLMIQEQLKVMFVGGPNTRKDYHIREGERVFYQLBGDM
1	l		VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
1	1		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS
1		1	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHFREL
!	1		QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
1			VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
l .	ł		DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
1			YCRCVPHRPAHCCHPPSCPSOPRCHAPGRAAAPHLLWOTOPTAL
I			
5392	1	1.000	PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	ı .	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACKPR
!			CAMPCPLPALSRCRGAGSRGSRGSRGAAGSGDAAAAAEWIRKGS
1			FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
l			RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1			GMSISIHISTDCLSLSVPATRQVIANHHMPSISFASGGDTDMTD
I			YVAYVAKDPINGRACHILECCEGL\AQSIISTVGQAFELRFKQY
1			LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
I			GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
l			PGDGYVQADARGPPDHERHLYVNTQGLDAPEPEDSPKKDLFDMR
ĺ			PFEDALKLHECSVAAGVTAAPLPLEDOWPSPPTRRAPVAPTEEQ
1			LROEPWYHGRMSRRAAERMLRADGDFLVRDSVTNFGOYVLTGMH
1			
l			AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
6303			SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			\nLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
		j	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
			QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
			STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
5394	2	982	RAPTDDDKNIYLTLPPNDHVNSNN
5394	- 4	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIOWFHNG
		ĺ	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
		ļ	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
			SQKFSHLDPTFSIPOANHSHSGDYHCTGNIGYTLFSSKPVTITV
			QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1		1	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
		1	RAPTODDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLINTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
			SSGNPEAVALAPDAYSTGSSSASSTLKRIKKPRPPSLKKKOTIK
		i	KPTETPPVKETQOEPDEESLVPSGENLASETKTESAKTEGPSPA
		l	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1		[SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
		ł	PRSPARPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
		Į.	PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
- 1		ĺ	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
			YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			ALVNTAAKNOHPVPRGI APNQESHLQVPEKSSQKELEAMGLGTP
- 1			SEATETTAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYSESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
			\SLADLFRRYEKMKEVLBGFRKNEEVLKRCAQEYLSRVKKEEQR
- 1			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5396	3135	531	RASDAKNOBGLINTRRKSTDSVPISKSTLSRSLSLOASDFDGAS
			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
(1	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
- 1			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
- (PRSPARPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
i			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
- 1			YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE
J			ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
l l			SEATETTAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
- 1			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
			PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
Į.			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
5397	3135	531	CRV\DALBRTLEOKNKRIBELTKICDELIAKMGKS RASDAKMORGLLNTRRKSTDSVPISKSTLSRSLSLOASDPDGAS
3331	3732	531	
- 1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGRVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
- 1			
	!		
	!		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptic
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E:
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, N=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PQQSYMFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAM
			AMGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQL
		ľ	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKO
		l .	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPC
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEET
		1	ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGT
		i e	SEATEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAE
		!	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQ
		ł	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVA
			YEKTIAQMIEDBQREKSVS\HQTVQQLVLEKEQA\LADLNSVE
			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAGEYLSRVKKEEG
			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVPSADPTARPSETNFDGTKLDI
			HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCV
	1		ILDSQTVVLKEFQCILGRLSEKSSG\QM\AQKFSFFPGFLGPF
			TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGT
	1		ENIRILPRILNVLFDSLQERLYTKMNLKPHRSRBYLRLSSEQE
		ļ	EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESI
		ĺ	DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKF
	ł	ł	MLRLSQDVKGYSFIKDLQWIQVSDSKHAYRLLKLGIKHQSVAI
			KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSE
			TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFOOH,
			FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKI
			AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVK
			ATISWENSLEDIMEDEDLVEELENAEETED/VGETKLLDEDLD
	1		TLEENKAFISHEEKRKLLOLIEDLKKKLINEKKEKLTLEFKIR
	j		EVTOBFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLV
	1		KCDTREEAAKDICATKVETEEATACLELKFNOIKAELAKTKGE
			IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIII
			KEDTINEFONLKSHMENTFKCNDKADTSSLIINNKLICNETVE
			PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQB
	ł		SEEVRPNIABIEDIRVLQENNEGLRAFLLTIENELKNEKEEKA
			LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVC
	i .		SKNOEGEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRT
	l	}	DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKO
			KEYRIQEPNRENSFHSSJEATWERCKEIVKASSKKSHQIEELE
	ĺ		QIEKLQAEVKGYKDEMNRLKEKEHKNQDDLLKEKETLIQQLKE
			LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETIL
			TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKN
	{		KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETE
			LKEELSASSARTON\LNADLQRKEEDYADLKEKLTDAKKQIKQ
			QKEVSVMRDEDKLLRIKINELBKKKNQCSQELDMKQR\TIQQL
			BQLINQKVERAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQ
			EQDQVL\BAKLEBVERLATELDRWRVKCNDLETKNNQRSNKEH
			NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKE
	l		BNIRNKEMKKYABDRERFFKQQNEMEILTAQLTEKDSDLQKWR
	l		ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQ
	I		MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCE
	ĺ		STENDOSTREPKPELRIOFTPLOPNKMAVKHPGCTTPVTVKIP
	l		ARKRKSNEMEEDLVKCENKKNATPRINLKFPISDDRNSSVKKE
	l		KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQH
	[PSILQSKAKKI IETMSSSKLSNVEASKENVSQPKRAKRKLYTS
			ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSODOINEYKECFSLYDKOORGKIKATDLMVAMRCL
			ASPTPGEVQRHLOTHGIDGNGELDFSTFLTIMHMOIKOEDPKK
			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFR
			\ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVPEVQKV
	1		QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQ:

Second Predicted Predicted end Designating Signat Septiming Designating Designating Designating Designating Designation				
Docation cortesponding to first anino acid a	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Location corresponding to first anino acid amino acid residue of sun acid amino acid residue of sun acid amino acid sun acid amino acid sun acid su				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid reinted of servine of first amino acid reinted of servine of serv	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
Lo first amino acid acid amino acid acid acid acid acid acid acid acid				H=H1Stidine, I=Isoleucine, K=Lysine,
amino acid residue of senione of the service, T-Threonine, X-Valine, senione ocid sequence describe, T-Threonine, X-Unknown, **sicop Codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide deletion, codon, /-possible mucleotide, codon, /-possible, codon, /-possible, codon, /-possible, codon, /-possible, codo				
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and acquence Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion FRWSFBHTTHALBUNGCYTHOUSY EDITORISE FRWSFBHTTHALBUNGCYTHUS FR				WaTryptophan VaTyrosine Vallebroom 4.Cha-
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:			Glutamic Acid, P=Phenylalanine, G=Glycine,
1	location	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	seductice		\=possible nucleotide insertion)
1			RNLVFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
	ľ		SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
i			CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLPKCKECGKSFCMLSHLAQHKIIHTRVWFCKCEKCGKAF
1		1	NCPSIITKHKRINTGEKPYTCEECGKVFNWSSRLTTHKKNYTRY
1			KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS
1		Į.	NLTEHKKIHPGEKPYKCEECSKAFNWPSTLTKHKRIHTGEKPYT
ļ		1	CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL
1		1	TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE
			KCGKAFNCPSIITKHNRINTJEKPYTCEECGKVFNWSSRLTTHK
		1	KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
1		ł	AFKWSSKLTEHKITHTGEKPYKCEBCGKAFNHFSILTKHKRIHT
1			GBKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ
J	J	J	SSNLTTHKKIHTGGKPYKCERCGKAFNQFSTLTKHKIIHTEEKP
1			YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST
1			LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC
1			EECGKAFNYSSHLNTHKRIHTKRQPYKCKECGKAFNQYSNLTTH
1			NKIRTGEKLYKPEDVTVILTTPOTFSNIK
5407	3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETLMEQGKGLAVLIL
1	1		AIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF
İ			KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1	(YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
		i.	QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
1			HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
1			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
1			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
1	Į.		LVQBLWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
J			LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
į			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
ì	1		EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSKQIL
1			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
			PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1 .			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1			DRAFIGNAYIAVDWHPTALHLRYOTSOERVVDEHESVEOSRRAO
1			VEPINLDSCLRAFTSEBELGENEMYYCSKCKTHCLATKKLDLWR
l i			LPPILITHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1			ALCOHKPLTPOGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1 1			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
1			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1 1			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
L			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
			HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
			APRPVPASRGGKTLCKGYRQAFPGPPAQFQRPICSASPPWASRF
			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLENKSMP
1			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
			NSSIQCVSNTQPLTQYF1SGRHLYBLNRTNP1GMKGHMAKCYGD
			LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
			LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
1			
			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i .	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TOTOFSSSPSTNEMPTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
Į.	3		NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
1		1	PSLFGMPLIVPCTVHTRKKDLYDAVNIQVSRLASPLPPQEASNH
1		1	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1	l	l	DRAFIGNAYIAVDWHPTALHLRYOTSOERVVDEHESVEOSRRAO
			VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
			LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1	i .		ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
i	1	ļ	VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
ļ			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
	ļ		PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
	1		VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLNDIAGQERFG
Į.			NMTRVYYREAMGAFIVFDVTRPATFEAVAKNKNDLDSKLSLPNG
			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
i			BNINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
-			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
	i		GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQPN
			GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
-		1	QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
1	ľ		KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
1			DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
			KPA\FEBFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI LNGGPS\NROTNGCLNGYTPSRKROASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
3412	3100	313	KMEGESSRPEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1			NEQSQITERKKEKKDFQHLISSPLKKSRICDETANATSTLKKEK
1			KRRYSALEVDEEAGVTVVLVDKENINTPKHFRKDVDVVCVDMS
1			IBQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
l .			KAASWESQRA\RDTLPQSEPPTQEESWLSVGPGGEITELP\ASA
1			HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMORSOPTV
			GLDDETPOLLGPTHKKKSKKKKKKKKKNHORFESLAMPEGSOVGS
Į.			EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKKSNHQEF
1			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
J			SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
ì			VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1			LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
1			KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
			KKMFDVNNYKGRYSEGDTEKLKNYHSLLGNDWKTIGEMVARRSL
			SVALKFSQISSQRNRGAWSKSETRKLIKAVBEVILKKMSPÇELK
			EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
			KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI
			DWEDLASAIGDVPPSYVQTKPSRLKAVYVPFWQKKTFPEIIDYL
			YRTTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
			SEGGGHRERERPREHAMFTPVIPVLMEAKAGWII
5413	3753	1304	RPPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
			TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
			HPFPKBIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
			TVBIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
	l l		KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
			IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
			SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
			VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF
			VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHRIPVFIAMGVV
			GGVLGAVFNALNYWLTNFRIRYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
			* *** *** O SEPROSES I PROTECUPO INSUMALINIPER

[and	I 5 - 12 - 2 - 2		
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
_			SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
1			SLLIGAAWGRLFGISLSYLTGAAIWADFGKYALMGAAAQLGGIV
1		ľ	RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKI/GDVFIEGLYDM
1	1	l .	HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
1	ļ	1	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
j i			FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECIMD
			LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPDRCVSTETGRRDRARVPS
			QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
	1	l	AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCOGPRGTRSP
			RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNYMDRFTV
			AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
1			RKYLMCGGTAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
		ł.	STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD
1 1		ł	MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
			NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
			RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
1 1		ĺ	SRRLRHSNPRADPLVCATGLIGSAPFLFLSLACARGSIVATYIF
1 1		1	IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
i 1			AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLM_CAFVGALGG
5415	693	2986	AAFLGTAHLH
1 2412	0,53	2906	IPPKTKLELQKH\LTTLT\NQBQATIFEEVQKLRPRNEQRENEL IISPLRCLPBEKQKBHIHIGEMKQTSQMAAENIGSELPPSATRF
			RLDMLKNKAKRSLTESLESILSRGNKARGLOEHSISVDLDSSLS
1 !		1	STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE
1 1		ľ	EPAPLSPOOAFRRANTLSHFPIECOEPPOFARGSPGVSORKLM
i I			RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWROOIFL
] :		l	RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
1 1			EKKRTSRELRELWQKATLQQTLLLRMEKENQKLQASENDLLNKR
1 1			LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
1 1			GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
l 1			SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
) J			VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM
			IILQIQNYQLSRLLHDYHRDLYNHLBEH3IGPSLYAAPWFLTMF
1		1	ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN
			LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
			VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
			AKPSDREPECTOPEPTGD
5416	27	4074	KSOLFCFWGGKAGDILSGDODKBOKDPYFVETPYGYOLDLDFLK
1			YVDDIQKGNTIKRINIQKRRKPSVPCPEPRTTSGOOGIWTSTES
1			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
			ENROLPPPSPQLPKHNLHVTKTLMETRRRLEGERATMOMTFGEF
			RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
			SYAPAAPTTSSMCSSIRHSPLSSGISTFVTNVSPMHLQHIREQM
			AIALKRLKELEBQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
i			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
			TVEQSTORIKBFROL\TADMQALEQKIQDSSCEASSELRENGEC
			RSVAVGARRNMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
i			AMLGVMTEADKRIELQQQTIESLKEKIYRLEVQLRETTHDREMT
			KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
' 1			
			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELFMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLMLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
			MDLVDTCVGTSVETNSVGISCQPBCKNKVVGPELEMMWIVKER VEMHDRCAGRSVEMCDKSVSVBVSVCETGSNTEESVHDLILLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEGVHQFTKTKTPTLISSCTNTCLSTLDRQ
			NDLVDTCVGTSVETNSVGISCOPRCKNKVVGSELFERNWIJVERG VEMEDECGRSVEWCDKSVSVEVSVCETGSNTEESVIDLTLLKT NLINLKEVRSIGCGDCSVDVTVCSFKECASRGVWTEAVSQVEAAV MAVPRTADQDTSTDLEGVHQFTRTETATLISSCINTCLSTLDKQ TSTQTVETETTAVOKGERVEDINSSTKTESIGVOTLISSGERGEPR
			MOLVOTCVOTSVETNS VGISCOPECKNIKVVSPELENNIKVIKER VEHEIRECAG SVENCKOKSVEVSVECEGOSITESSVIDLITLIKER VEHEIRECAG SVENCKOKSVEVSVECEGOSITESSVIDLITLIKER NIMLIKEVRS IGCGGCSVDVTTCSFKECASRGVNTEAVSQVEAK VAMPETADDOTSTDLEGOVIGITIKTHETALIE SECINTICLISTLDKO TSYGVVETRIVAVGRERVEDINSSYKTES IGVOTILISGISGFOP SAVYTKRESVOQININNIMIYLIGHKETILAGEPQLITVOLITASR
			NDLYDTCVSTSVSTRSVGISCOPECKNKVVGELIPRINNTIYEE VEHEDRCAGSVMCDKSSVSEVSCTGOSTTSSVIDLTLIKT NIALKEVRSIGCSUDVTVCSPKECASRGVNTEAVSQVEAAV NAVPRTADQTISTLEGUVAGPTINTSTATLISSCHNTCLISTLEK TSTUTVERITUAVRIGELVGLINSSTKTRSIGVTLLESSGSGFOB PSAVEKKESGVGGINTINDSYLVGLIKRETIACGPPCLITVGLTASR REVGVGDDPGVGSLENPFOPDAJOMNTCLIBNTETROKLLAGGO
			MOLVOTCVOTSVETNS VGISCOPECKNIKVVSPELENNIKVIKER VEHEIRECAG SVENCKOKSVEVSVECEGOSITESSVIDLITLIKER VEHEIRECAG SVENCKOKSVEVSVECEGOSITESSVIDLITLIKER NIMLIKEVRS IGCGGCSVDVTTCSFKECASRGVNTEAVSQVEAK VAMPETADDOTSTDLEGOVIGITIKTHETALIE SECINTICLISTLDKO TSYGVVETRIVAVGRERVEDINSSYKTES IGVOTILISGISGFOP SAVYTKRESVOQININNIMIYLIGHKETILAGEPQLITVOLITASR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid recidue of amino acid sequence	Producted end nuclectide location corresponding to first amino acid residue of amino acid sequence	AMAINO acid segment containing signal peptide (A-Alanine, C-Cyyteine, D-Aspartic Acid, S- Glutamic Acid, F-Phenylalanine, G-Glycine, E-Histidine, L-Iocaleucine, K-Lystee, L-Leucline, M-Methionine, N-Asparagine, L-Leucline, M-Methionine, N-Asparagine, L-Leucline, M-Methionine, N-Asparagine, S-Gerline, G-Glutamine, R-Asparine, S-Gerline, G-Glutamine, N-Asparagine, N-Cytesiane, N-Tyrosine, N-Mikhowa, *-Stop M-Tyrytophan, Y-Tyrosine, N-Mikhowa, *-Stop M-Tyrosine, Y-Tyrosine, N-Mikhowa, *-Stop M-Tyrosine,
5417	27	4074	ISQLE-PRINGSRADTISGEQUERGROPFY FETTY SYCLOLOPIE. YPODICKNIT INCRINATION GRARES PROFESSOR INSTITES LSS BRIGONYCOPPILATION OF CREATER PROFESSOR INSTITES LSS BRIGONYCOPPILATION OF CREATER PROFESSOR INSTITES LSS BRIGONYCOPPILATION OF CREATER PROFESSOR INSTITES LSS BRIGONYCOPPILATION OF CREATER PROFESSOR INSTITUTE OF CREATER PROFESSOR INSTITUT
5418	24	1133	HIMPARAGSPOPPELCERTS POPTHROSSD SPERAGRIMETAGAELTOPALLEG LOUVENTOD FLEVILF OF TAY STOPPALLER PED MARCH POADAGAUT, OVERTOPHMANGODEKE KTOPPALLER PED MARCH POADAGAUT, OVERTOPHMANGODEKE KGLÜBEKKIR BEREARTVSAAAGER POPTPOPELE TED STYTEL DEHGEVERVÖP DES VERMANGSGERÄP PORVADAGARVOR DEP TI DEHGEVERVÖP DES VERMANGSGERÄP PORVADAGARVOR DEP TI DEHGEVERVÄNDEN STANDEN STANDEN TENEN STANDEN STAN
5419	1395	259	GYBPLOPDIAVSSTSVGGBLYTFACKONSSTIESSFFLGIVARLE BE SESANCKAPGHOESEBEGGRASTOFGGASSKIHTANHETPERJAA KOPASLPGC/LOF/DCVR-PAQPESSKYCSDOCOMIKLAANETYSELL PORTCOMOGO STCLABBENKKLLEBETREGGGARTELGOMERSEFF BLEAT LIDANQQAVKROESSHEDDBODTD/LITCVSCGHETNER BLEAT LIDANQQAVKROESSHEDDBODTD/LITCVSCGHETNER BLEAT LIDANQQAVKROESSHEDDBODTD/LITCVSCGHETNER CONSTRUCTION OF THE STANDARD
5420	117	1733	NEAGGACPFKGGASGRIYLSPRIPRVSVAGCBERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

Destinating microcotide location corresponding to first amino acid anino acid acid acid acid acid acid acid acid	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Note				
Cortesponding Coffeeponding Coffeepondin		nucleotide		Glutamic Acid P-Phonelalanian C.Clusies
Cortesponding to first amino acid residue of serine, Gedlutamine, R-Arginine, Pepoline, Gedlutamine, R-Arginine, Seserine, T-Threonine, V-Valine, serine acid sequence		location		
to first anino acid an	1			
amino acid red.dus of roddus of sequence series, T-Threeonine, V-Valling. W-Tryptophan, V-Typosible mucleotide deletion, V-Typosibl				
residue of amino acid sequence (amino acid sequence code, "First Code," yeopsible mucleotide detector, 'Apposible mucleotide detector, 'Apposible mucleotide detector, 'Apposible mucleotide objection, 'Apposible mucleotide detector, 'Apposible mucleotide insertion'	1			P=Proline, Q=Grutamine, K=Arginine,
amino acid sequence Codou, /=possible mucleotide deletion,	J			S=Serine, T=Threonine, V=Valine,
Sequence				W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
BOTISTILIARILYILDI ILIPATERIKERARETY GOMMENDESTELL LILELCTPILALGANILLIPS I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI GOMMOS TYSHYO TARENTA PONISI I ISWALLISLEPINYI GOMMOS LIIGIANILYE PONISI I ISWALLISLEPINYI LIIGIANI EAARPIANGOTSI GOVER PRINCIPATI VINA PARALITI CLUKTIFTAN TAREL RARPERS SARIA TARENTA PONISI I ISWALLISLEPINYI GOMMOS LIHGIANLIYE PINISI I ISWALLISLEPINYI TORINOS TARRA PINISI I ISWALLISLEPINYI TORINOS TARRA PINISI I ISWALLISLEPINYI TORINOS SYSSILISLEPIN TORINOS TORINOS TORINOS TORINOS TORINOS TARRA PINISI I ISWALLISLEPINYI TORINOS TOR	1		sequence	
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I.SCLISOWKSVI.SPGSAADPSICS ISASSTGSSLDGHGERAEPRG GSILAWISSILLGEPTQERSGWINGEPT ROTS SQUINGERGAEPLG GRRISFQAETWACVLIDDSLIPS FDGHS PLINFINKETEDLLIDT YPLEFGOLDFULLDSKYADPVLIDGSVIDLSGFVSPARTIKEP				
GSLAKVSSSLEPVPQREPSSVYGLGPRFQMSPQPVFSGCDASGL GRRLSFQAEYMACVLPDSLPPSPDRHSPLNIPNKEVEDLLDYT YPLRPGPQLFKHLDSRVPADPVLQDSGVDLDSSVSPASTLKSP	1			
GRRRLSFQABYWACVLPDSLPPSPDRHSPLNNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP	1			
YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP		j		
	1 1			
INVSVMCPVARATALPFSGPREPSLKCWPSRVPQCGGMGLASW				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
J	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	- codeomec		SQLASTPRAPGSRCARWERREPALRGAKDRLTIGKHLDMGSPOL
			RTRDRGWPSPRPBREKRTSQSARRPTCTESRWXSEEEVESDDEY
ı			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
	i	1	PASFPSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1	l	ł	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
1			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
			SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLOCLLE
i	1	ĺ	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
			DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLNLGVTLP
			NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
			ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
1			AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
1			KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1		1	YQAPVSVMPVATSDQBGDSSFGKYGRNALRVAALCRGPRCLPTA PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
1			NCSWEVAYLPSBAGSLIF
5426	42	3435	ATSSOSLGRADPPROGTMERSPGEGPSPSPNDOPSAPSDPTDOP
1			PAAHAKPEPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA
i .			GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEOL
1			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
J	!		LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1			KBQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1	[EPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
1			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
ł			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
			PQWGETYEVNVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
1			VSSRPDPPSAAILVVYLDRAQDLPNVTSELYPPQLKKGNKEPNP
1			MVOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1			KDDSRALTLGALTLPLARLLTAPELILDOWFOLSSSGPNSRLYM
1			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPORGSSVDAPPR
J			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
[[VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVFGQELEVEVF
	1		DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
			ERLTPRPTAABLEBVLQVNSLIQTQKSAELAAALLSIYMERAED
1			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
			RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	[[GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGOVKLTLWYYSE
1	1		ERKLVSIVHGCRSLRONGRDPPDPYVSLLLLPDKNRGTKRRTSO
1			KKRTLSPEFNERFEWELPLDBAQRRKLDVSVKSNSSFMSREREL
		A	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
[-	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDBEQL
1			TAKTLYMSHRELPANVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
			EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGOEIEVEVFDKDPDKDDFLGRMKLDVGKV
1			LQASVLDDWFPLOGGOGOVHLRLEWLSLLSDAEKLEOVLOWNWG
1			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVOV
			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
			KLVMRILYLDSSEICFPTVpGCPGAWDVDSENPQRGSSVDAPPR
)			PCHTTPDSQFGTBHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRS FRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	,	\=possible nucleotide insertion)
			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
	Į.	ļ	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
i			RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
1	1		SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
1	l	l .	GGPPHITSSAPEV\RQRLTHVDSPLEAFAGPLGQVKLTLWYYSE
			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSO
1			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
1		1	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAESLED
	-		LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
1	ì		LAASIPYPHAMFINDMMECKODEIVMOGMDPSALEALINFAYNG
]			NLAIDQQNVQSLLMGASPLQLQSIKDACCTFLRERLHPKNCLGV
1			ROFAETMMCAVLYDAANSFIHOHFVEVSMSEEFLALPLEDVLEL
1			VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
	ĺ		FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
			AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
ł			CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
ļ			WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
1			TDKWTVVISMSSNRSAA\GVTVFEGRIYVSGGHDGLOIFSSVEH
1 :			YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
1 .			AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
			TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
1 1			I
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
			AQRERFHRFQPTYPYLQHEIDLPPTISLSDGREPPPYQGPCTLQ
i l			LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS
1			GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
			LEGTRLHHTHIAPLESAAIWSKEKDKOKGHPL
5430	441	1507	QKRRKRRRKKIMKTIOPKMHNSISWAIFTGLAALCLFOGVPVRS
1 1			GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
1 1	,		GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
, ,			HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
1 1	ĺ		TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A
1 1			APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
1			EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
i i			CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
			HLLLKF
5431	2	1312	AAAAPGSRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
1 1			LPGITIMP\TIAEGPSP\TSEGASEANLVDLOKKLEELELDEOO
1 1			KKRLRAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
]]			GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1 1			SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
1 1	1		YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1	J	J	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
30			DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
		j	AMAIFELLDYIVNBPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
		J	DLKMLTNHTFIKRSEVBEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQO
1 1	1		KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1	1		GLIMARKLIHLBIKPAIRNOIIRELOVLHECNSPYIVGFYGAFY
1 1	1		SDGEISICMEHMDGGSLDQVLKEAKRIPREILGKVSIAVLRCLA
	1		YLREKHÇIMHRDVKPSNILVNSRGEIKLCDFGVSGOLIDSMANS
	1		FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
	1	1	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
	l	1	AMAIFELLDY IVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
	J	J	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVQFEDPLHLCSWRARACPCTWPEC/CTGLLECLGPAGV
	l	1	LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
	J	j	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptid
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
NO:	nuclectide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		1	IAFTSAGSAVLLFLAMPMLTIGGILFLITMLQIGNLFGQHRST:
			ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLbhlhlcLqylac
			STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QOLSMK
			GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVW1
	i	1	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTOFGVI
	1		CAPWNGLLMDRLKOKYOKEARKTGSSTLAVALCSTVPSLALTSI
	1		LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAF
	1	1	SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLONDPFYVNVM
	1	i	MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSG
5151	1	032	
	1		HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
	i	1	LRQGRFGMFIGCINYPECENTELIDKPDETAITCPQCRTGHLVQ
			RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
			AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPINVTLSSGFVADRGVKF
		1	HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSS
	1	1	GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAN
	1		TQKSSNSLVFQTLFRHMRRRAMSHNVKRLFRRLQEIAQKEAEK
	ļ		VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAN
	l		RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLODLSYYCCLE
			LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
	ľ	1	KYPREMLGPVTFIWKSQRTPGDPSESROLWIWLHPTLKCDILER
	l	1	IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKKK
			KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMENN
	ł	l	RFRLIGPLSHSILTEALKAASVHTVGEDTEETPHRWWIETCKKF
	l .		DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
- 1	[ĺ	PACAN DEPENDENCE AND AND AND AND AND AND AND AND AND AND
	1	l	KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
	l		TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
		ł	TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
- 1	l		SQYKRS PNVPGDFPDCPAGNLFAEEQAKNLLEKYKRRPPAKRPN
			YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDI
			RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
i	ĺ		PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
- 1	1	1	RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
i	i		PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
- 1	ſ		KKREKROKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
			HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSOPAAO
			RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCOWSLPERMPLVVFCGLPYSGKSR
2.50	1,01	035	
- 1			RAEELRVALAABGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
			ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
i			LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
- 1			GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1			SEKSAKHGSGAFYSPRLLEALTLRFEAPDSRNRWDRPLFTLVGL
- 1			EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
			QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMABLSRLRR
1			QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHT?AMFLRRLGGWLPRPWGRRKPMRPDPPYPE
1			PRRVDSSSENSGSDWDSAPETMRDVGHPKTKDSGALRVSRAASE
- 1			PSKBEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
- 1			WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEXPGRREKLLGWLR
- 1			GEPGAPSRYLGGPERCLQISTNLTLHLLELLASALLALCSRPLR
- 1			
- 1			AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1			CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG
5438	0.00		KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
	1		LAPPSLRRPMMCQSEARQGPELFAAKWLHFPQLALRRRLGQLSC
1	J		MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
- 1	i		DI-HHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D-Aspartic Acid, E=
NO;	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine,
ĺ	corresponding	to first	L=Leucinc, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1		l	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
1		I	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
			LAPPSLRRPMMCQSEARQGPELRAAKNLHFPQLALRRRLGQLSC
1		(MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1		1	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1	Į.		DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGOVK
1			NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
1	Į.		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1			GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
İ	ĺ		FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
			MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1		į	FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
			ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKFLEIKTQCSGPRMDPKICPADPAFFSFIN
	ļ		NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
ľ			FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
1	l		ALBERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
			LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
	i		PPALFIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
1	1		DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
		ĺ	SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
(YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
1			KLSGPDDDPLHKQPRFWASMMEAAKIPHPHTRSDVRLYGMIYKP HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
			AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
1			GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
1 1			AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
			GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
1 1			HSIRCPESGEHYEVTLLHFLOEYL
5442	1	3474	CGQRSRRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPPKEAPAR
			APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1			KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
1 1			HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL
1 1			ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
1 1			IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
! !			KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK
1 1			PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
			KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL
1 1			TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
			AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK
1			NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
1 1			GSLSAKLNFLEIKVRYVPKQ\RPPKIPLGFASGGKTSENAD/IV
1			VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE
1 1			KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
1 1		1	DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
1			RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
1 1		l	TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
1 1			LVEYCLEGSERWYPANTEPVERCGFTVKNLPTGARILFRVVGVN IAGRSEPATLAQPVTIREIARPPKIRLPRHLRQTYIRKVGEQLN
1			
1 1		l	LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
}]	1		NALVEWQAPKDDGNSEIMGYFVOKADKKTMEWFNVYERNRHTSC
1 1		1	TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
1 1	1		PFEYKEHDFRMAPKFLTPLIDRVVVAGYSAAINCAVRGHPKPKV
1 1	j		VWMKNKMBIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
1 1			NELGEALAECKLEVRVPO
-			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ .	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	sequence	*possible nucleotide insertion)
5443	66	1003	
5443	1 66	1003	SRGQLDAGQSSRQHGGNRQPRQSRSRSSSSSSSSPRRSRSAAEPA
1	ł	ł	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
1		ŀ	LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
1			NKIEEFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
1	1		RFEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
1	l .		KFLDGNEWTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
l			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHOVKSRLLKEVS
i			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
	_		RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
1	1		
j	ļ	l	IKVEAADMARAKALLGGPGERLEADTEYLDPFDAQPHPAPPDDG
1	t .		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
1	1		QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
1	1		SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
1	I		SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
1	i .	1	LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
1			*PDWGDRRPNGQVATGLPELNGAEAPSAAAHPGLHRERHPEGLP
1	1		RABKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH
1			QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVBICIOLPLPASEPVLLLTWARRRWRETRSRREPT
			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
i		1	EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSOAHSTLKLANH
1	1		QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
1			ACROSCOT CORTO DE DESENSO CRANDOS CARA PEGCENOSE P
ĺ	1		ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
1	1		QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
1			DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
1	1		QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1	1		ALPGQPLPGASVRGLHPVQKVILNYPSPWDQRERPAQRDCSFPG
			LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
			PPSNPPARGTLKTSNLPEBLRKVFITYSMDTAMEVVKFVNFLLV
Į.			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
1.	1		DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRFIPVLF
	[PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLREEEYVAPPRGP
i			LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTERKYELKEGO
0	7.2	101	TLDVKCDYTLEKFASSQKANQIIRDGEMPKTLACTERPSKNSHP
			VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
			MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
1	ľ l		TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
1			GGFLSKSLVFSVLPAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
			KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGOOKDTSGVAR
1 .			PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
1			GSCPSQRLQWPGKEPQVTFPIKEFSCSSLWTSHVPASHMPLAAA
1 '			RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
1 .			TPRRIRGROALSTETGKGKDVEPCGPPAGRAPAPLYVGPGVSEF
1			IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
1			SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
1	1		GFSSEMKAWDIRTGKVMRSYKATIOOTLDILFLREGSEFLSSTD
			ASTROSADRTI IAWDFRTSAKISNQIFHERFTCPSLALHPREPV
1			FLAQTMGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
)			GDLLVTGSADGRVLMYSPRTASRACTLQGHTQACVGTTYHPVLP
			SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
			KSPSPSKSLLVLLOGRAMFQPATCPWQLPALSX
5448	194	1833	MASKVTDAIVWYOKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1 1	i 1		HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
1			RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
1	i		GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKKLRKAAHLEV
1			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
)			GSKKAKNGIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
	J		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nuclectide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł.	amino acid	residue of	S-Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /mpossible nucleotide deletion,
l .	sequence		\=possible nucleotide insertion)
			IRPBETAWNTGTLRNGPSKDTQRTITNVSDEVSSEBGPETGYSL
			RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1			QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHOINPC
Į.	l .	Į.	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
1		ŧ	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
[1	
)	1	ļ	TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
		1	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
	I	1	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
ł	1	ì	SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
i	i .		VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
	Į.	1	LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
į.	l .	1	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQRBIKGLRNKPKKTA
1		1	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
1	1	l	RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
		į.	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
1			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPOCET
	1	į.	IRPEETAWNTGTLENGPSKDTORTITNVSDEVSSEEGPETGYSL
1			RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
			QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
		l	VKKEYRDDPFEQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
1	1		VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
1		[TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
1	i		FFFLLCVAERTYKQVGIM*TSBGVLRNRKSHHYKKHYPNEDAPK
			SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
1			
1 .	i		SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
l	1		VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
			LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
			PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
			LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
1	l		YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
i			VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
	1	í i	RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
	ł	ł	HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
			HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA
	l .		AGCRLEREEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPGL
ł	l		PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK
1 .	1	J	SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
	1	1	GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
	1	Ì	HIIPPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
1)		SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
ì			VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
1			LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAENWATQ
i			AFHORDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQBILSNL
j :	l	l	SFPVTIORATVWMLRLEPLHTONTOQETLTTAHLEATLEEAGPS
			PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYGA
1		1	TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
1			LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERFRLGRLAWRG
			TODKTTMVTSPTNEDLLRGRLVYQHDDSETTEDDIPFVATROGE
]			SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
			TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
1			TOEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
			AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
			SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
			RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
			LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
			GVLVELEVLPAAIPLEACNFSVPEGGSLTLAPPLLRVSGPYFPT

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, CaCysteine, D=Aspartic Acid, E-
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H-Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q-Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	l	\=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1		1	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQP?ILT
1	1	}	TNTGLQMWEGATAPIPAEALRSTDGDSGSEDLVYTIEOPSNGRV
1			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
1		ł	TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVOPLSSOTLRASS
			SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTCAEVYA
1	1	1	GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
1			AACPQRPSHLWKNKGLWVPBGQRARITVAALDASNLLASVPSPQ
i		i	RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGOLV
1	1		YAHGGGGTQQDGFHFRAHLQGPAGASYAGPQTSEAFAITVRDVN
			ERPPOPOASVPLRLTRGSRAPISRACLSVVDPDSAPGEIEVEVO
1			RAPHNGFLSLVGGGLGPYTRFTQADVDSGRLAFVANGSSVAGIF
1	1	1	QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPOALGRSSL
1			SOCOLRVVSDREEPEAAYRLIOGPOYGHLLVGGRFTSAFSOFOT
1	1	ĺ	
1	1		DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV WAGGPWPQGATLRLDPTVLDAGELANRTJSVPRFRLLEGPRHGR
1			VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
1	ľ		AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
1	(ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
1	1		IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
i			GDTETFRKVERGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
-			ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
			KNSEPGSPHSLEALRDAAPSQGLNFLLLPTKMLFIFNFLFSPLP
	1		TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
i			PYRWLSYKOVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPRW
1	1		IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
1			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
1	1		YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHON
1			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVONE
1	1		AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIODSL
			GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
i	1		FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
			TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
i	[1		KNIFKLAQGEYIAPEKIENIYNRSQPVLGIFVHGESLRSSLVGV
1			VVPDTDVLPSFAAKLGVKGSFEELCQNQVVRBAILEDLOKIGKE
1			SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYPRTO
1			IDSLYEHIOD
5452	1833	1138	SRVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
1	1000	1130	LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
1			HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEBRSS
1	1		
1	1		VTIKVTIIIYLSILGLLLYMVYLTLVEPILKRRLFGHAQLIQS
1	1		DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
EAES	111		RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
1			AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
1			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
1			VRFYDSWBSTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
l	1		RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
ì]		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
I	1	1	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1	1		EGCIRONKDERYSIKOLLNHAFFQEETGVRVELABEDDGEKIAI
1			KLWLRIEDIKKLKGKYKDNEAIEPSFDLERNVPEDVAQEMVESG
1	1		YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPOSAPPEPHREETVTATATSOVACOPPAAAAPGECAV
			AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
	1		POSERSQQQDDIESLETKAVGMSNDGRFLKFDIEIGRGSFKTVY
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q-Glutamine, R=Arginine,
	amino acid residue of	residue of amino acid	S=Scrine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
J	sequence	padaetica	\=possible nucleotide insertion)
-	boquanos		VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKTKVL
1	1	Į.	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
	i		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1	(LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
		l	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
1	1		KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQENVESG
		L	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCL3VFGLFRLIQ
1			WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
1			GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
1			-QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1	1		KALLPSMIKRRQGHIVAISSIQGKMSIFFRSAYAASKHATQAFF DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
	1		TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
1			LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACC
	1		TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
1		l	QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
1.			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1		ĺ	DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
1)	EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
			ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL QBLKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
1		ľ	SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFESIA
1			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
			ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDILATGTRKG
i			QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
!			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
		ĺ	SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
5457	2	1540	MSMYRVRGGRVAGGCFIGWRAPCPRATK
5457	-	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSAERLMRKVKKLRLDKENTGSWRSPSLNSEGAERMATTGTP
			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1 :			APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
J .		i	RKEALLLLSWKOMLDHFQATPHHGVYSREEELLRERKRLGVFGI
1 '			TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1 1			PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
]			RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
1			EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
			GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPDECPAVCGVRGGHORLDOCS
5458	6642	4022	PVPGLREPOWEPAOPSATMSAPSHEEEYARLVMEAOPHWLRAEV
	****		KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
			VRKVLELQTELKQLRNVLTNTQSENERLASVACELKEINQNVEI
			QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
			VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
			LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
			DLISELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
			SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
			DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
()			HARRIGRYBARGQALTEKVSLLEKASRQDRELLARLEKELKKVS
	ļ		DVAGETQGSLSVAQDELVTFSEELANLYHHVCNCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPBAGRA
			DGGTGDS8PSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
1 1			
		1	AAVDRTTELSRQRIASOELGPAVDKDKEALMEETLKLKSLLSTK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Nethionine, N=Asparagine,
	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	Doguonoo	\=possible nucleotide insertion)
			REQITTERTVLKANKOTARVALANLKSKYENEKAMVTETMMKT.R
1			NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
1		Į.	KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
		·	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNENDIVKQGYVRIRSKRLGIYQRCWLVFKKASS
1			KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
}	Į.		GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
1			DLLATGVEREQSERFNYYLMPSPNLGCYMGECALQITYEYICLW DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
1	į .		OTROGEALYOKVHSAALAIAEOHERLLOSVKNSMLOMKMSERAA
			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
			PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
		i	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
			GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
ļ	1		ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
i			CEKCHHFFVVLSBADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
1			KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
			VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
1	l·		AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
1		l	VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGBGVQQGLLKLLEG
1			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
İ	ĺ		NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
1			LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
l			NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
ì	1		IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
5461	1481	160	SEEEYDSGVEBEGWPRQADAANS
3401	1401	100	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
	1		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1			NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1 !			ASTRLPPTPLLLFPEERATNGREGLLRFSSWPFSIQDVVQPLTL
			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
	' '		BANBBFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
1 1			QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
			TGCVDLTTTNILEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
5462	663	3353	TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA
1 5102		2223	RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILOLIT
1	1		SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1	1		CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
1			VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
			WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
1			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
			NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
1 1			SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK RHYWRLDSKCLTLFONESGSKYYKEIPLSEILRISSPRDFTNIS
			QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAOS
			WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCGIOE
1 1			NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
l i			RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
1 1	l l		LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
1 1			DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
1			LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
1 1			QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
			WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNI,VYP KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTWTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
		20-2	YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
			PLVEWLENPGPQHEKETLFGDMVCFLFITPLATISGWLCLRGAV
			DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
	1		RTNORVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHOYVHKTFYEEYOTTL
			GASILSKIIILGDTTLKLQIWDTGGOERVRSMVSTFYKGSDGCI
	1		LAFDVTDLESFEALDIWRGDVLAKIVPNEOSYPMVLLGNKIDLA
1	1		DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
	1 5275	2240	VMVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
1			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
			KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
	{	[RLGTYESDKAMTVYECLSEKGQILCAICPNPXLVITGGTSTVVC
	1		VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1			DRTCLIWDLNKLSFLTOLRGHRAPVSALCINELTGDIVSCAGTY
[IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNBWDTQNVIVTG
1			HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
			DEDSSDSEADEQSISQDPKETPSQPSSTSHRPRAASCRATAAWC
1			TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGGTRAHLQGPLSHP
1			HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHPA
!			EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
			GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
1	1		SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIOTSPVLLASLGVGLVTL
1	_		LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
1			RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
)			YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
			AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
1			FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
]			QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GRALRVGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
1 1			RSPRKIDOFCNSSNMVHGSVTFRDVAIDFSOEEWECLOPDORTL
1			YRDVML3NYSHLISLAGSSISKPDVITLLEGEKEPWMVVRKETS
			RRYPDLELKYGPEKVSPENDTSEVNLPKOVIKOISTTLGIEAFY
1 1			FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT
]]			HKPYECKECGKYFSCGSNI-IQHQSIHTGEKPYKCKECGKAFQLH
			IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
			BCKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
1 1			QHQKIHSNEKPFVCKECGMAFRYHYOLIEHCOIHTGEKPFECKE
			CGKAFTLLTKLVRHOKIHTGEKPFECRECGKAFSLLNOLNRHKN
			IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
1			FNRGAHLIOHQKIHSNEKPFVCRECEMAFRYHCOLIEHSRIHTG
)		DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
	1		LOLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF
1 1	1		ECKECGKAFRLHMHLTRHQKLHTGEKPFECKECGKAFRLHMQLI
!			RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SPLTDLFQSLAQLENLCKQLYETIDTTTRLQAEKALVEFTNSPD
1 1			CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEORIDI
1		J	RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
	,		RNAITDVTRFLQDSVEYCIIGVTILSQLTNBINQVSATAFLIBA
	1		DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKOASGKNLNLND
	ł	,	ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
1 1			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
1 1	1	ľ	SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
	1		VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
ı I			KSSKLYRRLSEVLGLNDRTMVLSVFIGKIITNLKYWGRCEPITS
1 1	I	1	KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
1 1			QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
	į.		AVAQMFSTNSFNBOEAKRTLVGLVRDLRGIAFAFNAKTSPMMLF
	ľ		
	ı	I	EWIYPSYMPILQRATELWYHDPACTTPVLKIMAELVHNRSQRLQ

SEO	Predicted	Dec 21 2 2	The state of the s
ID ID		Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	Doquoneo	\=possible nucleotide insertion)
			FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
1			TOT CHOME AND CONTRIBUTION AND AT MANY COMPANY OF THE PARKETS
			ISICFSMLKAALSCSYVNPGVFRLYGDDALDNALQTFIKLLLSI
i			PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
ľ	í	1	ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ
!	1	ļ	ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
			LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
			TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
			EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
	1	ľ	VPENNG3AGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
	1		EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
			IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAO
1	1		CYNTTWSEWSPSTKWHNSYREPFEOHLLLGVSVSCIVILAVCLL
}	1		CYVSITKIKKENWDQIPNPARSRLVAIIIODAGGSOWEKRSRGO
i			EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPPQGSGK
ſ			SAWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEEEKG
Į.			SPCACEPSCED DEOPCRETURE DESCRIPTION OF THE SECOND
I			SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKBQPLHLEPS
1	ļ		PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG
1		ĺ	PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
1	1		LQHGAAAAPVSAFTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
1	1		YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
i	1	ľ	PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1	1		KPPLPQZQATDPLVDSLGSGIVYSALTCHLCGKLKQCHGQEDGG
1			OTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
1			STAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
			RVS
5470	17	1413	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPNSDF
ĺ			KNVGLVFVNSKRDRTKAVLCMVVAGATAAVFHTLIAYSDLGYYI
J	l .		INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1	1		SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
	1		LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
1	ſ		LILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1			YGWLTEIRAVYPAFOKNNPSNKLVSTSNTVTARHIKKFTFVCHA
			LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
1 1			PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
1			
			GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT
5471	1868	658	EGEDSANTOMPPTEZVTDIVEMREENE
34/1	1000	658	RSSAPPGPQRAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV
			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGNVSSAYDHVR
1			KTRVAIKKISPFBHQTYCQRTLRBIQILLRFRHENVIGIRDILR
1			ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
]			GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
1			HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
1			NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
1			PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
1 !			YLEQYYDPTDEPVAEEPFTFAMBLDDLPKERLKELIFQETARFQ
			PGVLRAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
1 1			DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWOGDTFHR
1 1		1	GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
			VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA
1			"ATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
1 1		1	VGTMLPCFCPTEQALALV
5473	- 3	2119	
1 24.5	,	2113	PMNVKLLIQDLBDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
	1	J	KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS
1		J	FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT
1		J	LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
			TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
1 1			LLRRHTBFFSQLDQRVLMAFLKACDELTDILPEQEQQGLQBAVR
			KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence	-	\=possible nucleotide insertion)
			KLMPQE3SEKIIKEHRVFFSDKGPHHLCEKRLQLIEELCVKLPV
	í		RDPVRDTPGTCHVILKELRAAIDSTYRKLMEDPDKWKDYTSRFS
			EFSSWISTNETQLKGIKGBAIDTANHGEVKRAVEEIRNGVTKRG ETLSWLKSRLKVLTBVSSENEAGKQGDELAKLSSSFKALVTLLS
	1	}	EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQARKILDTE
			NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
ļ			HEELRKLESTLDGLERSRERQERRIQVTLRKWERFEINKETVVR
1			YLFQTGSSHERFLSFSSLESLSSELBQTKEFSKRTESIAVQAEN
			LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYVIDK
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
ĺ			LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
			QECRDTQPFDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT
			LCDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS
			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
\$475	2	506	ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF
)			VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
l .			STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
5476	192	1457	GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR
3475	192	1457	SDSMSLLDCFCTSRTQVBSLRPEKQSETSIHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPTGTL
			VTIKITNLENCNEERLKALQKAVILSHFFRHFNITTYWTVFTVG
			SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
1			YLHQNGCTHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
			AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ
			SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVOLC
			LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI
5477			SLPPVLPWTEPBCDFPDEKDSYWBF
54//	3	1044	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI
1			VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFQGALTMKQVMPSKRLDHLQRAREHFINYLTQCHCYHVAEFE
1 1			LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELB
1 1			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDO
			EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA
			GYPSLPTMTVSDWYEQHRKYCALPDQGIAKAAPBEFRKAAQQQB BQEEKBBEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
\$478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGOSFVTASDDKT
			VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
			LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
			DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
			MEGRLLYTLHCHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVFRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
			LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRAHTAIVRSVHFCSDGQSFVTASDDKT
	1		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
1 1			LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGNDNTVKVW
	1		DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGBYFASGGSDEQVMVWKSNF
	1		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
			LENQQLIMQRATP
5480	444	1952	LSLTSRMEEABLVKGRLQAITDKRKIQEKISQKRLKIEEDKLKH
	1		QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI
	1	ſ	LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEONR
[[1		KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGO
			KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH
1			BPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
			HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
Į.	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	boquonec		LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCOE
1	1		DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
			GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
1	1		TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLLHESPQPPALRV
1			VATSSDRWFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
ſ			QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
ì	ł		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
1			YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
1			ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
			LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
1			KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGLLWT
			CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
			QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
5482	1492	528	AKGKSVFLDQMKKFVEWLQNABBESSSEGEEN THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
3402	-172	J**	EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
1			CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDROLPSFOTFFAPA
1			LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACCNVTLEVSTGP
			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
1			IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
i			TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
			VMVPAQSQAGSLV
5483	1	788	PFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
1			ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
1 .			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
			FEVOLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
1 1			EIRINNLKSELSROKLHTOELLSQLEMANEKVAENEKLILEHOE
5484	3	1997	KANRLQRRLSQASERAASASQCLSVITVQRRKAASLMNLENI IMADMEDLFGSDADSEAERKDSDSGSDSDSDOENAASGSNASGS
3.01		2001	ESDQDERGDSGQPSNKELPGDDSEDEGASHHSGSDNHSERSDNR
1 1			SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
1			AEGSEKAHSDDEXWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
1			LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPVA
[SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
1 1			EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
1			NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
1 1			DBFEDBEMLDEEGRIRLKLKVENTIRWRIRRDEEGNEIKESMAR
]]			IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTOKIRILPMAGRD
1			PECORTEMIKKEEERLRASIRRESOORRMREKOHORGLSASYLE
1 1			PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
1			EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTOEPTALNEELTDO
			AGTN
5485	161	1074	KRKILSSMMDSBAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
	ļ		CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
)			RGILPPLMOKTT?LALMFGLYEDLSCLLHKHVSAPEFATSGVAA
			VLAGTTEATFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
	1		GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLFTATTHSAHLVN
) J	ļ		DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFQKI
5486	1404	142	NLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
2400	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
]]		,	GGLAGG TGOMUNIFICAGE AND PROPERTIES OF THE TOTAL CONTROL OF THE TOTAL CO
			GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV IPGLKGYVAERKGERBEMQDAHVILNDITEECRPPSSLITRVSY
1 1		j	FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
1 1	J	!	LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
		J	DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
		ľ	DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SRQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ACDGLFKVFTPBEAVNFILSCLFDEKICTREGKSAADARYEAAC
1			NRLANKAVORGSAENVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
ļ			LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
			CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
1	1	l .	GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
			LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
ĺ	Ĭ	i	NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
1		Į.	FNPAPAIADLDPQFYTLSDVPCCNESEAEILTGLTVGSAADAGE
			AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
5489			TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
1	ĺ		LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
l			IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNBEQYCGDFDSF
1			FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
			NLPEAQEKNEEEGSTATEETBEIAMEGAEGEAEEEESTAEGEEP
5490	81	893	GEDEDS
3430	61	89.1	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
			LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
)			IAGDEDNRRWMRENUPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
			PSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
			NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
1		2271	QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
1			LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKYGNCNTPKP
			SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
i			PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
1			ITKAIKSKNVDVNVKDEBGRALLHWACDRGHKELVTVLLQHRAD
1			INCODNEGOTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
1			EEVTGCKTVSLVLORHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYRATEE
1			QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDOETALSAM
1			RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP
			IDPEDAPESITRAVASLPPEGMFELMKQMKLCVQNSHQEARNML
1 1			LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
) [SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
			PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1			VGPVPLKRGQVQMSDPRAPIPRGPVTPGGLPPRSLLGDAPNDPR
1 1			GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
			GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
1 1			VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
1 1			MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
			GTGMQGAGIQGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1 1			PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQS1
5493			LILKEQIQKSTGAS
5493	1	1876	RAPMNTKAVPEEPRKPGRLTQALNSPLTWEHVW1CVPGGTPDCL
1 1	1		TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
]]	. 1	j	VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
1 1	1		EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
1 1	1		EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
1 1	I		GSALLSLSRSVQELTRENQSLKEDLDRVLSTSPTISKTQGYVEW
1 1	ſ		SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
1 1	i i	1	HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
1 1			QAKADLEKBLECAREGEBERREREEVLREEIQTLTSKLQELQEM
			KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEGLPRP
			RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bodanioc	\=possible nucleotide insertion)
	bequence		(=possible nucleocide insertion)
1	1	1	GHLTRIKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
į.	Į.		PVQEEATVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
1			HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
-			SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
1	i		RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
1	1	1	PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
	_	1	GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
i	i e	1	ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
		I	QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
	ĺ		GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
1	ł	ł	LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
	l	ł	SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
1	ſ	i	CTVWTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASO
1	l	J.	
1		1	KIRKLESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
1	l	1	GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
1 .			LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
		1	PRFDHLVATERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
1 1	1	ı	IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
			VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
			WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
_		l	AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
			MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
			SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGOKPSSSDTFFR
1			FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
1 1			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK
		l	SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
i l			MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
			LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
1 1			MKRSSSOMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
			TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAOENHDDLMS
i l			VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
			NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLO
1			
i i		i	CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
1 1			KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
1 1			GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
1 1			ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
5497	1821	2200	HHIKKMTVE
3497	1021	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1 1	ì		CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
1 1			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
	ļ		YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
(1	ļ		PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
) 1	ļ		LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
	J		DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
1	ł		STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRSTIGAGPIPIK
1 1			TPVIPVKTPTVPDLPGVLPAPPDGPEERGRHSPESPSVGEGPOG
[[VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER
			EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
			TINDRSAPRES
5498	2434	1492	
-150	**34	1492	ILTHQBIFTGEKPCBCGKASIQMSHISQQKIYSGENPFACKVCG
1 [KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYV1KHQNTH
			TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
			QKSNLIRHQRTHTGEKPFVCKRCGKTFSGKSNLTEHEKIHIGEK
1 1	1	ĺ	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNBOGKAFSQRTS
			LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
1			
			NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEO	1 2 2 2		
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	[A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			OKIHTH
5499	324	926	GFGQICRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
1			FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
1	i		WKVRMFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
1		1	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
1	i		PPERWOKLESVLPPERLPVOREEE
5500	1.978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDPKIEHTWDGFP
1			VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
i			DYEVVEAFFLNDITEQYLEVELCPHGOHLVLLLSGRRNVWKORL
1	1	ľ	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
1		i	YEALYPVPQHELQQQQKPDFHCLEYFKSFNFNTLLGEEWKOPES
í			DIWLIEKCHI
5501	2927	2226	
3501	2341	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
l .			AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
1	l .		SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
			CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
ł	1		NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
			LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
1	1		GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
	1		REIALAKKHGTONKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
ì			REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
			EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
1	1		TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD
Į.			IKQLAAWAT
5503			
5503	216,	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKKVDOATKSTA
5503	216.	654	KGVRRKGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA EKVLVLRFGRDEDPVCLOLDDILSKTSSDLSKMAAIYLVDVDGT
5503	216.	654	EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDOT
5503	216.	654	EKVLVLRPGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AVYTQYPDISYIPSTVFPFNGQHMKVDYGGEDPALRSIKAVRRT
5504	216.		EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTLGEKPVNS
		654 3563	EKYLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT AV TYQYFDISYIFSTVFFFNQQHMKVDYGGEDPALRSIKAVRRT SPAGTLGBKPVNS QLSFSFQAPVTFDDITVYLLQEBWVLLSQCOKELGSNKLVAPL
			EKULVLERGREEDPVCLQLDDILSKYSSDLSKWAAIYLUDVDOT AVYTYYEDISYIPSTVFFFNOQHMKVDYGGEDPALRSIKAVRRT SPAGTLGBKPVNS CLSSFQAPVTFDDITVYLLQBEWULLSQOOKELGSNKLVAPI GPTVANPEJFKRGRGPEPBULSVQQGRSLLEHFPGKKKMGYMG
			EKVLVLREGRBEPVCLQLDDILEKTSSILSKMALIVLDVDOT AVTTYPEISTISTETSFTFENGHKVDVGGEDFALRSIKAVRT SPAGTIGBKPVNS OLASSFORPYTFDDITYYLLGEBKVVLLSCOKKELGGSNKLVAPL GPTVANTEL-FRKPGRØFENILGSVOGORSLLEHHGKKMOYMG BREVGGPTPSSOGSLPFOKKYLSHLSTGSGEHIEGDMAGRYRKL
			EXULVARPORDEDPUCQLIDDILSKYS SIQLSKMAAI YJUVYDOT AVYTYYTSILYTSETVFF PROQHMKVDYGGEDPALRS IKAVART SPROTLOBKRVNIS QLSFSPQAFVTFRDDITYYLLÖSEKVLLSQCOKELCGSNKLVAPL GPYVANDE JRKERGROEPENIGSVQOGRSLLESHIPOKKQKOYMG BMEVQGTTRESGOSLPPOKKAYLSHLSYGSGHITGUMAGRIKKL LKPRSICKSKWYQFVENIKNIKGTALFGSAGKYST IRDKSGRI
			EKUMLURBERBEDPUCLQLDDILSKTSSDLSKWAATYLDVDOGT AVYLYYDEDIST, DETVFFRYGGBHKVDYDGGBDALRS ILAVART SPASTLGSKEVMS OLSFSFQAVTFDDITVYLLGSKRVLLSOOKSLGSNKUNAPL OPTVANBELFRKFOROPEPHLGSVQGGBLLGSHKKKKKKKKKYKYK BEBVQGPTBSGGLEPDKKATILSKTGSHIEDDMAGSNKL LKPBSTQKSHFVQFHLINKBSCHLSCGASKEVFSTBOKSSKL LKPBSTQKSHFVQFHLINKBSCHLSCGASKEVFSTBOKSSKL LKPBSTQKSHFVQFHLINKBSCHLCGASKEVFSTBOKSSKL LKPBSTQKSHFVGFHLINKBSCHLFVALASABUPTARARESTER
			EKVUMLNEGERBEDVECLOLDGILSTSSDLESMAAIYLINDVOOT AVYLYTEDISLTSTSTPERGENWAVOORGDEALGERAVART SPAGTILGEROWIS OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI OLISEPGOPATEDITYYLLOBENVILLSOOKSELCISNELVAPI LEGATOPEKVETLINGUASSALMENCVALLAMADDITAARERSIL DENTYOPEKVETLINGUASSALMENCVALLAMADDITAARERSIL DENTYOPEKVETLINGUASSALMENCVALLAMADDITAARERSIL
			EKUMLINGGERDIPUCLUDDILSKTSSDLSKWALTUNDVOOT AVYLYTED SLT BYTFFRYGGBHKVDYGGSDALRS ILAVART SPASTLGSKEVMS OLISFSQANTFIDITYVLLIGSERVLLSOOKSLCGSNKUNPL OPTVANRE-FRYGGREPBULGSVQGGRELLESHEKKKOKSTYM BENVQFPTESGOSLEPPEKASTVGGRELLESHEKKKOKSTYM LKPBSTQKSHFVQFPHLINKESCHIELGTGSHEEDMAGSNKL LKPBSTQKSHFVQFPHLINKESCHIELGTGSHEEDMAGSNKL LKPBSTQKSHFVQFPHLINKESCHIEVANLAARDPTARARERSIT DPHGULASFERLEYNLAKSKHHWCNIALARDPTARARERSIT DPHGULASFERLEYNLAKSKHHWCNIALARDPTARARERSIT DPHGULASFERLEYNLAKSKHHWCNIALARDPTARARERSIT DPHGULASFERLEYNLOGTLOFTWOMTHOMINGHOOTHINGHAVE DPHGGUALTHULGTSLAKKSTTOMTHOSTUNDAVIS
			EKVUMURBERBEDVECLELDDILSKYSSILSKWAAIYLINDVOOT AVYNTYPEDISTE TSFFFRENGHWAVDYGGDEALER, ILAVERT SPACTILGERUMS GOTVARHELFERFESSEPPHLGSVOORELLGSNKLWAPL GOTVARHELFERFESSEPPHLGSVOORELLGSNKLWAPL LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER LCHASIOCKSWYDIPWLINKEEDTALCGAREFFSITOKESER EDPOGOOAITWAYLOCISOLINGKSTTOCHASSIATL EDPOGOAITWAYLOCISOLINGKSTTOCHASSIATL EDPOGOAITWAYLOCISOLINGKSTTOCHASSIATL EDPOGOAITWAYLOCISOLINGKSTTOCHASSIATL
			EKUMLURBEREBEPVELQLDOLLSKTSSDLSKWAALYLIVDVOOT AVYLYTPOELST DETVFERGGBHKUVDYGGSDPALRS IKAVART SPAGTLGSKEWAS COLSFSPANVFFDITVYLLGSERVALSOOKSELGSSNKUNAFL GPTVANRE-FRKFGROPSPHLGSVGOGRELLERHERKKKOMIYM BENQCPTESSGOSLPPOKKASTUSHELGTGGBHERDMAGENKEL LKPBSJCKSHFVGFPHLINKBSCOMLECGACEFYSSTBOKSSRL LKPBSJCKSHFVGFPHLINKBSCOMLCGACEFYSSTBOKSSRL LKPBSJCKSHFVGFPHLINKBSCOMLCGACEFYSSTBOKSSRL LKPBSJCKSHFVGFPHLINKBSCOMLCKALARDPTHARRERSIL DPAGUNLASPERLSTADCFTFYPEDIGGGFSKAELLFSSKAEL DPAGGUALTRAVLICTSLAURKSTTGAHSSDKTTLYTMAVS SCIQUESABGLSEEVFVYFEDIAVYTEDIAVYTTEEBGOOLDKS GKELYBDUWFMSTLLASIGFAARKOLDLSKEERGAMIKKOPS GKELYBDUWFMSTLLASIGFAARKOLDLSKEERGAMIKKOPS
			EKUMLURGEREBUPUCLLUDILISKTSSILISKMANIKUNVOOT AVYTYTEDISLISTETSFPROMENVOTOSIDBALEILIAVERT SPACTILISKEVMS SPACTILISKEVMS GOTSVARTESPROMENVOTOSIDBALEILIAVERT SPACTILISKEVMS GOTSVARTESPROMENVILOSEKVLLSOOKELCUSNKLVAPL GOTSVARTESPROMENVILOSEKVLLSOOKELCUSNKLVAPL GOTSVARTESPROMENVILOSEKVLLSOOKELCUSNKLVAPL LKDRSIOKSKYVOIPHLINKESCUTALCSACKETYSI TRUKSSRL LKDRSIOKSKYVOIPHLINKESCUTALCSACKETYSI TRUKSSRL LKDRSIOKSKYVOIPHLINKESCUTALCSACKETYSI TRUKSSRL LKDRSIOKSKYVOIPHLINKESCUTALCSACKETYSI TRUKSSRL LKDRSIOKSKYVOIPHLINKESCUTALCSACKETYSI TRUKSSRL EDOGGODAI TRAVILOLISIDENVETTOSIINSSDLTIILINKALVE SCLOPENSALISEKVAVINSELUSPANAKTIOKISKSUTALINKALVE CKELTYDVORNENVELLASLOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVELLASLOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVELLASLOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVELLASLOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAAKPOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAARIOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAARIOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAARIOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAARIOLISKLERRAAPIILKOON OKRIKTUDVORNENVENTAMELOPAARIOLISKLERRAAPIILKOON
			EXCULARGEMENDIPUCLUDILISTS SULSAWAN YUNDYOOT AVVITYPED STYLET STYPEPROMEWOYDOGDDALAGE HAVENT SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACTILGENEWAS SPACE SPA
			EKUMLURBEREBUYCULLDOLLSKISSLISKANALYLINVYOOT AVYTYTEDISLISTETFFPRENGHWYVOTGGDERLAG, ILAVERT SPACTILGERWINS COLSFSCAPATFOLGERWINS COLSFSCAPATFOLGERWINS COLSFSCAPATFOLGERWINS COLSFSCAPATFOLGERWINGSVOGGELLGESNELVAPL GOPTVARFELFERGSGEFPRILGSVOGGELLGESNELVAPL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL LADESI OKSHFVOJFHLINKESCUPLICAGERFYSI TRUGGSBL EDDOGODAL TRAVILLCIS LIDENZETT TOUTGSBL EDDOGODAL TRAVILLCIS LIDENZETT EDDOGODAL TRAVILLONZETT EDDOGODAL TRA
			EKUMLURGEREBUPUCLUDDILSKYSSULSKYABIYLINDVOOT AVYLYTPEISLY ETSTYFPENGHWUVDOGDDALGE ILAVERT SPACTILGERWYS SPACTILGERWYS DISFRYDAYPTPDITYYLIGBENVLLSOOKSELGISNKIVAPL GERGARDE ZERGORDE PERILGS VOOGRELLISHERKKKONDTOR DISFRYDAYPTPDITYYLIGBENVLLSOOKSELGISNKIVAPL GERGARDE ZERGORDE PERILGS VOOGRELLISHERKKKONDTOR DISFRYDAY DISFRYDA ZERGORDE
			EKUMLURBEREBUPUCLUDDILSKTSSILERMANITUNVOOT AVYTYTEDIST, TESTFFFRENGURVOYDEGDEALER, ILAVERT SPASTILGEKUMS COLSFEYDAYTFDUTTYYLLOSEKVLLSOOKKELCOSNKLWAPL GUPTVARRES-FRKERGEPERMLGSVOGGRELLGERHERKKOMTUME BURVCEPTERSOOLEPOKKNITUNGENTALICGAECEFYSSIEDKSGREL LAUBSTOKSHFVOFFHILMENGENTALICGAECEFYSSIEDKSGREL LAUBSTOKSHFVOFFHILMENGENTALICGAECEFYSSIEDKSGREL LAUBSTOKSHFVOFFHILMENGENTALICGAECEFYSSIEDKSGREL DEPOGGOAL TAMWATULTSLAUBGURVANLAABED HINDARVS BURVGENTENTALICHARAKSKAMPUCNIALABED HINDARVS OKSLITUNGENTALICGAECHTSTOHIMSSIENKHINDARVS OKSLITUNGENTALICGAECHTSTOHIMSSIENKHINDAVS CRESTORIUMENTELLALGRAANFOLISCHERGAAPHLURG CRESTORIUMENTELLALGRAANFOLISCHERGAAPHLURG CSSIECEBOODERSIENTETPRESICHENOFFHILMENTALICGAECHTSTOHIMSSIENKHINDAVS DEFENTALICHENSSELIVE OFFVENTIKTERSKRIELCV NYUZIKEDTHAANFELDSALAKSHINGTERSALAKSHINGTEN
			EKUMLARGERBEDVECLELDDILSKYSSILSKYAAIYLINVOOD AVYLYTEDISLTSTYPFRONGHWAVOORDDALAGE HAVRET SPACTILGKEVMIS CHISTSGOAPVETBUTTYYLLGEEWYLLSOOCKELGSNELVAPL GUTVAMTELFERTORDEPBHLGSVGGGELLUSHICKKKONTIWG GUTVAMTELFERTORDEPBHLGSVGGGELLUSHICKKKONTIWG BEN OVGE TESSOOLD POKKNITIALINTSGOHEIDENGADNEKK IL BEN OVGE TESSOOLD POKKNITIALINTSGOHEIDENGADNEKK IL BEN VOOR DE SOOLD POKKNITIALINTSGOHEIDENGADNEKK IL BEN VOOR PERSON HER OVER THE STANDEN FOR THE PROGUNDARE STANDEN FOR THE PROGUNDARE PERSON HER PROGUNDARE STANDEN FOR THE PROGUNDARE PROGUNDARE STANDEN FOR THE PROGUNDARE PROGUNDARE STANDEN FOR THE PROGUNDARE PROGUN
			EXUMLARGENEDIVICALIDOTISTS SIGERMANIMOVOOT AVYTYTED IST STYPFPRONGHWYDYGGDENAGE IAWART SPARTIGERUMS SPARTIGERUMS GOTVANPELFRENGROPEPHLASVOGORALLESHRENKOMTUM GOTVANPELFRENGROPEPHLASVOGORALLESHRENKOMTUM BEWOGPTENGSGLEPOKKNITALENTSGRENGHOMAGNENKL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGARAFRESIS DPFGGGATARVALCISTALENGKANALARD FROMTANIMOVERSCHENGKANALARD FROMTANIMOVERSCHENGK
			EKUMLARGERBEDVECLEUDGILSKTSSILSKNAAT/KINVOOD AVVICYPEUSLE TEVFFPRONGENVOORDSALES (HAVRET SPACTILGKEWMS SPACTILGKEWMS GUISSFGOAPVETPDITYVILIGEKVILSGOOKELGUSNKLVAPL GUISSFGOAPVETPDITYVILIGEKVILSGOOKELGUSNKLVAPL GUISSFGOAPVETPDITYVILIGEKVILSGOOKELGUSNKLVAPL GUISSFGOAPVETPDITYVILIGEKVILSGOOKELGUSNKLVAPL GUISSFGOAPVETPDITYVILIGEKVILLSKSCHENGOOKELGUSNKLVAPL DEVOAPVETPDITYVILSKSCHENGOOKELGUSNKLVAPL LEGYTOP EKVETTLEVILASSCHENGOVALAADPD TVAABERSIT LEGYTOP EKVETTLEVILASSCHENGOVALAADPD TVAABERSIT EPOGUNASPELTATOOLT EVETPOGGOFBOKELGUSSKALE EPOGUDAT FRANTLOCISIOLOGUSTTO GUISSGOAPVETPOMARGES ECTOPEABLICEBEVOVETELEVILYBOAPVETPOMAVTET SERGOMLOK GUSSINGOOKE
			EXUMLARGENEDIVICALIDOTISTS SIGERMANIMOVOOT AVYTYTED IST STYPFPRONGHWYDYGGDENAGE IAWART SPARTIGERUMS SPARTIGERUMS GOTVANPELFRENGROPEPHLASVOGORALLESHRENKOMTUM GOTVANPELFRENGROPEPHLASVOGORALLESHRENKOMTUM BEWOGPTENGSGLEPOKKNITALENTSGRENGHOMAGNENKL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGERYFSIBOKSSRL LARBSIGKSHFVQFHILMRESGTALECAGARAFRESIS DPFGGGATARVALCISTALENGKANALARD FROMTANIMOVERSCHENGKANALARD FROMTANIMOVERSCHENGK
			EKUMLURGEREBUPUCLUDDILSKYSSULSKYAAT/KUVVOOT AVYTYTEDISLTESTYFPRENGURVOVOGGDALGERVAAT/KUVVOOT AVYTYTEDISLTESTYFPRENGURVOVOGGDALGERIAVRET SPACTILGERVWIS GOTVARRES-FRENGSDEPRILGSVOOGRALLESHERKKOKNYIVE GOTVARRES-FRENGSDEPRILGSVOOGRALLESHERKKOKNYIVE BERVOOFTENSOOLDE OOKKYSTOOTHENTSSEELE TO TOTGESER LOCASE OOKS VOO THIL INTERDITAL COARSET TO TOTGESER LOCASE OOKS VOO THIL INTERDITAL COARSET TO TOTGESER LOCASE OOKS VOO THIL INTERDITAL COARSET TO TOTGESER LOCASE OOKS VOO THIL INTERDITAL COARSET TO TOTGESER TO TOTGESER EPROGOAT FRANKLOCIS DIALOGES TOTGESE DITALVINDAY EPROGUNAS PERENTALOCH TOTGESE DITALVINDAY OKROKKORP POER VERVOORT TOTGESE DITALVINDAY OKROKKORP POER VERVOORT TOTGESE DITALVINDAY OKROKKORP POER VERVOORT TOTGESE DITALVINDAY OKROKKORP POER VERVOORT TOTGESE DITALVINDAY OKROKKORP POER VERVOORT TOTGESE TOTGESER TOTGESER OOK OKROKKORP POER VERVOORT TOTGES TOTGEST TOTGESER TOTGESER OOKS OKROKKORP POER VERVOORT TOTGES TOTGEST TOTGES TOTGES OKROKE OOKS OKR
			EKUMLARGERBEDVECLUDDILSKYSSULSKYAATIANVOOD AVYLYPEDISLTETSTYPERMENDRYVOTGEDBALGELGAVERT SPACTILGERVWIS SPACTILGERVWIS OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKONDRY LEWBELD SENDEN PERMIGS VOLORISHE PERMIGS SEL LEGYROPE KULTURAS KAMMENUNALAMED PINARETSI EL DEPOGULAS PERMICS PERMICS VOLORISH VILLE VIL
			EKUMLARGERBUPUCLUDDILSKTSSILLSKMANIMUTVOOTD AVTYTYTEDIST JETVFFPRONGHWYDVOSTODALSKI LAVART SPACTILGERUMS SPACTILGERUMS GENEROPSE SPACE SPA
			EKUMLINGROEDSDIPUCLUDDILSKTSSILISKMAININDVOOT AVTYTYTEDISLTSTUFFPRONGHWVDYOGGDALGELGUNGKING SPACHTUGERUMS SPACTILGERUMS DENGTIGERUMS GENOCHTERSTUFFRONGHWINGSVOORBLEGSNELVAPE GPTVAMPEE-ERFORGOEPHILGSVOORBLEGENRELVAPE GPTVAMPEE-ERFORGOEPHILGSVOORBLEGENFORKOMDIVE GPTVAMPEE-ERFORGOEPHILGSVOORBLEGENFORCHTER LIKERSJOKSHYVJPHILMEEDTALCE APROLAAGHET SETOKESERL LIKERSJOKSHYVJPHILMEEDTALCE APROLAAGHET SETOKESERL LIKERSJOKSHYVJPHILMEEDTALCE APROLAAGHET SETOKESERL EPPGGOAT FRANTLOCTSDIPUCKTTOTHESSDIPUTLYMBAYE EPPGGOAT FRANTLOCTSDIPUCKTTOTHESSDIPUTLYMBAYE CORSINGEREVONDHERIKATOTHESSDIPUTLYMBAYE OKROMENDAMPHILDSTIPUTLYBDAY STATEMOLIUM OKROLANDHAMPHILASIAPAANFOLTSKLEREAAPHIKODH OKROMENDAMPHINAUSEAPHANFOLTSKAIRCV NEVERTORMONGHET STATEMOLIUM PERSTULLENTENTAUPESSDIPUTLYMBAYETANSTELME VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHESILIBUT VARIANCHVALUSSTIPUTLYBORGOEPHILMETHENDENTYVALLES TENTYFYOGSSKRIANELGEGOAPHILGELITELDILMANNINGER
			EKUMLARGERBEDVECLUDDILSKYSSULSKYAATIANVOOD AVYLYPEDISLTETSTYPERMENDRYVOTGEDBALGELGAVERT SPACTILGERVWIS SPACTILGERVWIS OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELLISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKKONDRY OLISFRÇANGE PERMIGS VOCORELISHERKONDRY LEWBELD SENDEN PERMIGS VOLORISHE PERMIGS SEL LEGYROPE KULTURAS KAMMENUNALAMED PINARETSI EL DEPOGULAS PERMICS PERMICS VOLORISH VILLE VIL
			EKUMLURGEREBUYCUCLUDILISTISSULSKWAAIYUMVOOT AVYLYYEDISLISTUSTYPERNGHWAVVOOTGODALGE IAVART SPAGTILGERWIS SPAGTILGERWIS OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME OLISFRÇANS DEPHLOS VOOGRELGISHEKKROOME DEPHLOS DEPHLOS DEPHLOS VOOR DEPHLOS DEPHLOS DE DEPHLOS DE DEPHLOS DEPHLOS DE DE DEPHLOS DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DEPHLOS DE DE DE DE DE DE DE DE DE DE DE DE DE
			EKUMLURGEREBUPUCLLUDGILSKTSSULSKWAAIYLINDVOOT AVTVYTEDISLTETSTFPERGEMINVOORDDALER, IRAVERT SPACTILGEROWIS SPACTILGEROWIS CHISSPEGNAPTEPDITTYYLLGEBUVLLSOOKRELGSNELVAPL GIFTVARTELFERGERDEPPLIGSVOORGELLGSNELVAPL GIFTVARTELFERGERDEPPLIGSVOORGELLGSNELVAPL GIFTVARTELFERGERDEPPLIGSVOORGELGSNELVAPL GIFTVARTELFERGERDEPPLIGSVOORGELGSNELVAPL GIFTVARTELFERGERDEPPLIGSSELGTSSELGTSSELGTSNELVAPL LEGEVIPPERVETLEVILASEKAMMENUNALABEPT VARABERSTEL ERGYROPEKVETLEVILASEKAMMENUNALABEPT VARABERSTEL ERGYROPEKVETLEVILASEKAMMENUNALABEPT VARABERSTEL ERGYROPEKVETLEVILASEKAMMENUNALABEPT VARABERSTEL EPPGGOATFRANTLOCISTURGEVETTOGITSSELTITYNENSEL EPPGGOATFRANTLOCISTURGEVETTOGITSSELTITYNENSEL ENGENGAMEN VARABERT VARABE
			EXCULARGEMENDIPOCLOLIDILISTS SILISMANI/LINDYDOT AVYTYPTED 17% TEVTFPPROGRAWINVOYSIGDBALES INJURAT SPACTILISTRAWS SPACTICISTRAWS
			EKUMLIKREGEBBUPUCLUDDILSKTSSILISKMANIKUNVOOT AVTVYTEDISLTETSTYFPRENGHWIVVOOTGODBLARE, HAVRET SPACTILGEROWIS SPACTILGEROWIS GUISSFORDATEDITTYVILIGERVILLISCHEKKONTIVE GUISSFORDATEDITTYVILIGERVILLISCHEKKONTIVE GUISSFORDATEDITTYVILIGERVILLISCHEKKONTIVE GUISSFORDATEDITTYVILIGERVILLISCHEKKONTIVE BUTTORIGHERT BUTTORIGHERT BUTTORIGHE BUTTORIGHERT BUTTORIGHE BUTTORIGHE BUTTORIGH BUTTORIGH BUTTORIGH BUTTOR
	Se	3563	EKUMLARGERBEDVECLUDDILSTSSULSAWAATIANDVOOT AVVITYPEDIST JETVFPERNGHWINVOORDDALAGE IAVORTE SPAATILGEROWS SPAATILGEROWS SPAATILGEROWS LOSSFROAD FERN ON OOR GOOGLEGESSENIA VAPI BEVORFTEN ON OOR SENT ON OOR SENT ON OOR SENT OF SEN
5504			EKUMLIKARGERBÜPUCLÜDÜLISKTSSILISKANALYILIVDYOÖT AVYTYTEDISLISTETPFRENGUNVEYDGÖDZILISLISHARAT SPARTILGERUMIS SPARTILGERUMIS DEN GERMEN EN STEPPER SPARTILGERUMIS DEN GERTENSEN SERVILGERUN LISSEN SERVILGERUMISLESHERKKONDYME GERVARPETEN SOOLIDE GERKATILGERUSKESTEN SERVILGERSEN SERVILGERUMISLESHERKKONDYME BEN GOPTENSEN SOOLIDE GERKATILGERTSSEN SERVILGERSEN SERVILGER SE
5504	Se	3563	EXCULURAGEMENDIPUCLUDILISTISSULISMAAIYUMVOOT AVYLYYDEISTISTUSTYPPROMENVOTOSIDALISII (HAVRIT SPAGTILISKEWIS SPAGTILISKEWIS SPAGTILISKEWIS SPAGTILISKEWIS SPAGTILISKEWIS SPAGTILISKEWIS SPAGTILISTISSULISMAAIYUMPUTOSIDALISII (HAVRIT GITVANTELISTICARUMPUTOTISTISTISSULISMAAIYUMPUTOTISSULISMAAIYALISSULISMAAIYALISSULISMAAIYUMPUTOTISSULISMAAIYALISSULIANAAIYALISMAAIYANIVAYYTYITISTIOOJAAIYALISSULITISMAAITAAIYAAISIAAIYANIVAAYTITIOOJAAINAAIYAAINIVAAYTISTIOOJAAINAAINAAIYAAINIVAAYTIOOJAAINAAINAAINAAINAAIYAAINAAINAAINAAINAAIN
5504	Se	3563	EKUMLIKARGERBÜPUCLÜDÜLISKTSSILISKANALYILIVDYOÖT AVYTYTEDISLISTETPFRENGUNVEYDGÖDZILISLISHARAT SPARTILGERUMIS SPARTILGERUMIS DEN GERMEN EN STEPPER SPARTILGERUMIS DEN GERTENSEN SERVILGERUN LISSEN SERVILGERUMISLESHERKKONDYME GERVARPETEN SOOLIDE GERKATILGERUSKESTEN SERVILGERSEN SERVILGERUMISLESHERKKONDYME BEN GOPTENSEN SOOLIDE GERKATILGERTSSEN SERVILGERSEN SERVILGER SE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of		S=Scrinc, T=Threonine, V=Valine,
ļ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence	 	\=possible nucleotide insertion)
1			YTMLRDSNATAAKKSLDVMIBLYRRNIWNDAKTVNVITTACFSK
!			VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1		1	KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
1		i	BKLLKQLBCCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
ì		I	FLOPHOREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
			NSGEVMTVGINAIKEITARCPLANTEELLQDLAQYKTHKDKNVM
			MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGELDAK
1	ł		DYIPGAEVLEVEKERNAENDEDGWESTSLSEEEDADGEWIDVQH
			SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM
[1	AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
1	ļ)	PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKOK
5506	1	1531	NFMMMRYSQMVRSKNKRSFREKQLALRDALLKKKKRMK
2500	1 *	1231	FRGDLCGCRGGSAPGEGGSSAWPAPAHPLPEREREALCPGRS
1		1	CSGGGGETPGTTPVWSPLEGGGDEELRPNPYVRFFYRWWAVVV
1			LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY
ł		l	LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
1			EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
İ			TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
1		l	SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIFVMLMGKLV
i	ľ		SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
1	ĺ		LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
1 .	J		LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
)			GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
5507	3704	1271	LRVYARGRLKQRGKKAVPVESPVQKV
3307	3704	12/1	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
	,		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
1	Į.		CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAZALCRSIRSS
1		İ	KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENENIMACY
[NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIZITSEDRFIQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI
1			GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
			ACAMAGATITAKKANGENTAGANAKTIPATGAGGAKTKHIASTIKAC
1 1	1		NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
			LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG
1 1	i		NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
1 1			FELEAATHNRPLIYLGLKNFARFGICEFLHCSESTLRSWLQIIE
1	1		ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
1 1	1		IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
1 1	,		QLTTGDDKCNIFKNMERNDYRTLROGIIDMVLATEMTKHFEHVN
1 1			KFVNSINKPLATLBENGETDKNQEVINTMLRTPENRTLIKRMLI
1 1			KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
1 1	1		FDRNTCSIPKSQISFIDYFITDNFDAWDAFVDLPDLMQHLDRNF
. 1			KAMKGIDEWKI'BUL'BABABA AND ALADPAD WORLD WALL AND ALADRANG AND AND ALADRANG AND ALADRANG AND ALADRANG AND AND ALADRANG AND AND ALADRANG AND AND ALAD
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
1	1	031	VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCOELREKFW
1 1	Í		
1 1			EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
5509	1238	619	KYRSPVPLTPPGCVALDTRAD RKSRGCQNALSASGPAAAAAAIMVRKLKFHEDKLLKOVDFLNWE
3300	1430	913	
]			VTDHNLHRLRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1 1	i l		ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
1 1			LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
5510	96	2200	EDFVTWVDSSKIKRHVLEYNEERDDFDLEA
2270	90	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
1 1	ļ ļ		AEGERQPPPDSSEEAPPATQNF11PKKE1HTVPDMGKWKRSQAY
1 1			ADYIGFILTINEGVEGEKETFEYRVSEAIEKLVALLNTLDRWID
1 1			ETPPVDQPSRFGNKAYRTWYAKLDERAENLVATVVPTHLAAAVP
	l I		
	í í		EVAVYLEESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
.			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
.			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI

Deginning mucleotide location corresponding to first and control corresponding to first and correspond	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation location corresponding corre	ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid R-
Location Corresponding C	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine
Corresponding Cofired Intel	1	location	corresponding	H=Histidine, I=Isoleugine, K=Lysine,
to first amino acid anito acid residue of residue of setious of se	1		to first	L=Leucine, M=Methionine, N=Asparagine.
ani no acid residue of maino acid sequence Seserine, T-Thronoline, V-Valine, Maino acid sequence Coden, /-possible mucleocide deletion. 5511 276 1980 KETYPTOPHEN, Y-TYPOSHOR, Y-TYPOSHOR, X-TUNION, *-stop Coden, /-possible mucleocide deletion. 5511 276 1980 KETYPTOPHEN, Y-TYPOSHOR, X-TYPOSHOR,			P=Proline, Q=Glutamine, R=Arginine,	
sequence sequence sequence (code, //possible mucleotide deletion, sequence sequence sequence (code, //possible mucleotide deletion). 5511 276 1780	1			S=Serine, T=Threonine, V=Valine,
anino acid sequence codon, /-possible mucleotide deletion, sequence 15512 276 1580 KISKURMIPPRILITESIAVPISQUEFENDEGAVELEERING KISKURMIPPRILITESIAVPISQUEFENDEGAVELEERING KISKURMIPPRILITESIAVPISQUEFENDEGAVERINERIAR TULOVITESIAVRISQUEFENDEGAVERINGERENDEGAVERINGEREN HARVITIONEGAVERINGERENDEGAVERINGERENDEGAVERILGEREN FOYEERIGSENSVELGEERINGERVEVVVGERANDEGAVERILGEREN SOFULALESSEN GALLERINGERVERANDEGAVERILGERENDEGAVERILGEREN SOFULALESSEN GALLERINGERENDEGAVERINGERENDEGAVERILGEREN SOFULALESSEN GALLERINGERVERANDEGAVERINGERENDEGAVERILGER SOFULALESSEN GALLERINGERVERANDEGAVERINGERENDEGAVERILGER SOFULALESSEN GALLERINGERVERANDEGAVERINGERENDEGAVERILGER SOFULALESSEN GALLERINGERVERANDEGAVERINGERENDEGAVERILGER SOFULALESSEN GALLERINGERVERANDEGAVERILGERVERANDEGAVERILGER VORGREDTOFFULAVRINGERVERANDEGAVERILGERVERALERINGERENDEGAVERILGER VORGREDTOFFULAVRINGERVERANDEGAVERILGERVERALERINGERENDEGAVERILGER VORGREDTOFFULAVRINGERVERANDEGAVERILGERVERALERINGERENDEGAVERILGER VORGREDTOFFULAVRINGERVERSOFFULARINGERVERALERINGER EINERFERDEGAVERVERANDEGAVERILGERVERALERINGERENDEGAVERILGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK STALLIUCOSPPELIOTARINGERVERSOFFULARINGER, DAPAK ROMENDEGAVERSOFFULARINGER,			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
S511 1980 KISRVINIPERMITTSIANVISQUESVADPGIATUSELDERUS	1		sequence	Codon, /=possible nucleotide deletion,
HESETEOUGNEIDATECH CHIEF TO THE CONTROL TH	L			
TULQU'IEDSSYNALSELPSGLPCKTUVESSE PRIVAKERIUG HIGHTI TIMI FINIKABAGHERUS IRNINGBORGE POLITOFOL FOYDERLOSSING AND THE HIGH THE THE THE THE THE THE THE THE THE TH	5511	276	1980	KLSRVLNLPPRNLITSISAVPISQKEEVADFQLSVDSLLEKDND
H.G. TIONFIANLES ALGREY TRIVING MOMERAPING VIDERAL STREET TO THE ALGREY TRIVING MOMERAPING TO THE ALGREY THE ALGREY TO THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE ALGREY THE	1	ĭ	1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
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				SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
í	sequence	noquenoc	\=possible nucleotide insertion)
-	pequence		HICPYRTNKYGEYYLLLLPGSYIINVIVPGHDPHITKVIIPRKS
1	l .		ONFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
1		1	KPSLFLFLVSLLHTFFK
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3515	0,	****	
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Ĭ			SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
			RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
1	i		IYPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYPSKKTGL
1	1		TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
1	ĺ		YVFIASIYLLGEKINHWKWVSVQILQRWRLESVGICFQWPDWKS
			PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAREDRPLEDVPQEAEGNPQPSEE
1	1		GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
			LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
i			WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
1	1	1	AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
			PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEEADEHL
			FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
			KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
i		ĺ	RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1		l .	ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
1			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1	1		VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
1	1		SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
į.			RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
1			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
1			CABTEFENGNRSNFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1	1		MAPFVRTLPTRPRWERIRDRPTFEMTETOFVLSFVHRFVEGRGA
ì			TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
Ι.			FLLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
			RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
l i			RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
			IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1 1			NLQNEAQCGHSADRHNAEAWKOTEPAEOKLNSVWIMPOOSAGLE
			RSAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTOVE
1 1			NMLYPKLISLNSAHFDFQGCNFSEKNNYARDRRDGQSKEGSGRV
1	1		AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPPA
1 1			FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
) }		RAWMLKHVRNSRGLESTLNVGVNKKRGLRTPPKSHNGLPVSCSE
1	[NTLSRARSFSTGTSAGGSSSSOONSPOMKNSPSFPFHGSRPAGL
J .			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	1.05	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRBSGS
1 -3.5		034	LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
)			VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
			SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD
1 1			LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
5526	3		TEDDMANYILNMADEAGQPHRP
3526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVIMLRVAWRTLSLIRTRAVT
]		QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
. i		1	LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
		J	KQEQFMKKIVANPEDTRSLBARIIALSVKIRSYEBHLEKHRKDK
ı i		{	AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
			YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAAQKQAK

SEC	Predicted	Donald shed on t	
ID		Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, 3=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Luquanos		RRNPDSPAKAIPKTLKDSO
5527	2005		
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
	1		KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
Į.			PAKNPSSLFSKEAFKRKAQAVSEEEEEEGKSSSPKKKIKLKKS
1	1		KNVATEGTSTQKEFEVKDPELEAQGDDMVCDDPEAGENTSENLV
	1		QTAPKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
l l		1	AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
	1	1	AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
1	1		AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
- 1	(VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEOTGN
	i		
	1	1	LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
- 1	ł.	1	FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
i	1		YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
i	1	ſ	RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
)	J.	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
			RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHOKORLRNLEO
1	1	l	FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
		l	RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVOTK
[1	1	YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
i	1	ŀ	EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESOKTK
1	í	ſ	YPTQSGKPPLLVSAPSKSESALSCLSKCKKKKKKKPKEPQPEQP
			QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
i i	ı		YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
1	1	J	QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
			FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
- 1	ı	-	LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLOGTL
1			AADKNEILFSEFNINYNNEPPMYRKGTVLIWOKVDEVMTKEIKL
1			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TERLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
5025	1	1	LSWILSRVLWLSGLSEPGAARCPRIMEEKALEVYDLIRTIRDPE
-			KPNTLESLEVVSESCVEVQEINEERYLVIIRFTPTVPHCSLATL
J	1	ļ.	
1			IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
			AAAMENPNLREIVEQCVLBPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
1	1		FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML
}	Į .		VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLOR
	1		DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
1	i .		QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
1			ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
1	1		PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTOVVLRRKPS
1			
1			VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
i			ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
- 1			TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
1			GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
1	1		LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
1	1		GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC
1			BKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSOPRAPRPRDSMERPEPELTROSWRAVSRSPLEHGTVLFARLF
1	(·		ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV
1	1		TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
1	1		
			LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMIIBDETBPCGEBLLHSVLQCKSVFDVLDGEBMR
	1		RARTRANPYEMIRGVPFLNRAAMKMANMDFVFDRMFTNPRDSYG
1	1		KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
1			GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDTTRPENISAFRN
1	1		FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
1	1		LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS
	1		RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL

SEO	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
: CM	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino agid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	
	amino acid	secuence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
	1		SEPROAEIRKECLRINGIPDQARVAPSSSDPKSKFPELIOGTEI
1	ł		DIFSYKPTLLTSKTLEKIRPVFDYRCHVSGSEQKFLIGLGKSQI
	1	1	YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
1	ſ	1	SATHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
	1		
1	ſ	1	PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
Į.	l .	1	VPMGLYIVRTVNBPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
i		1	IAPFHICYYGRLPWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
1		}	MHRA
5533	94	789	MKBRRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
			TVFENYTACLETREQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
i		1	LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
	1	ł	LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
1		l	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
1	1	i	MOTERIA PROPERTY PROP
			FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLBQRNLVTEVLGALEAK
1	i	1	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
1	Į.	1	AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
)	i		CAFILFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRINNDLSG
1	Į.		RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTODETOKSDSENEDLKIDCLOESOEL
	1		NLOKLKNSERILTEAKOKMRELTVNIKMKEDLIKELIKTGNDAK
1	ì	1	
Į.			SVSKQYTLKVTKLEHDABQAKVBLTETQKQLQELENKDLSDVAM
1	1	}	KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
	I		ELEQSVDHMKYQKIQLQRKLQEBNEKRKQLDAVIKRDQQKIKVI
			LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSFSRAPPPSAAPLPTGRAQMSP
ĺ			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVFTRAP
1			DAVYTELQPTSFTPTWPADETPQFQTQTQQLEGTDGPLVTDPET
1			HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGPHEDDPF
1			FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPOLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVART
		****	PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
1			ADMINISTER AND AND ADMINISTRATION OF A STATE
1			YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
1			YNKOLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEG
1			HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
1	1		FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1	[EKNYHCNNSEKTLNQSSSPKNHQENYPLEKQYKCKEF3EVFLQS
1			MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
1			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP
			TEEKPYKWKECGKVFNLNCSLYLTKOOQIDTGENLYKCKACSKS
I			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
I	1		EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
1			ON THEODIESCHED VICTORIA CONTROL OF THE CONTROL OF
1			SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
1	1		KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAF?YSSHLI
f :	(RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
			CGKAFSYSSDVIQHRRIHTGQRPYKCHECGKAFNYRSYLTTHQR
()	(SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
1	* 1		FSYRSYLTTHRRSHSGERPYKCEECGKAFWSRSYLIAHQRSHTR
			EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISOAOLSCTGPPAIPGIPG
1			IPGTPGPDGQPGTPGIXGEKGLPGLAGDHGEFGEKGDPGIPGNP
1			
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
			NVPLREDQTIEFDHVITNMNNNYEDRSGKFTCKVPGLYYFTYHA
1			SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
[GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
[]			IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
1			DELYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
1	i i		SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			BLBKVHDLCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY
ļ			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
ļ			RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
1		l	QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
5540	148	1440	LNLEGEWHYL
2240	140	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPNRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPNARRYDELPHYPGIVD
			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRKKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKÇVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
ĺ			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLFDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1	1		BDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
	1		LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
5541	148	1440	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
	240	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPMROHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
			GPAALASFPETVPAVPGPYGPHRPPOPLPPGLDSDGLKREKDEI
1	[YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLBLE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQMNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDGGVGLDTSVASPSSGGED
			EDLDQEPRRNKKRGIFPKVATNIMRAKLFQHLSHPYPSEEQKKQ
			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
5542	148	1440	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL PPLGAGAGVHARSPHPARRLPLTTAGVOGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDBLPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRP?QPLPPGLDSDGLKREKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
1			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
			Laqdtgltilqvnnwfinarrrivqpmidqsnrtqqgaafspeg qpiggytbtephvafrapasvgdefgtrkeewhyl
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
			KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
Į į			SSASRDRVLARTMIVADSECRABLKDYLRPAPGGVGDSGPGEEQ RESRARRGPRGPSAFIPVEEVLREGAESLEOHLGLEALMSSGRV
1			DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
1 1			ARHQCSYLVGSHMAEFLOTGGDPEWLLGLERAPEKLRKLSETNK
)]			LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
	1		SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSEDPLNNSGGF ESARDVBALMERMQQLQESLLRDEGTSQEEMESEFELEKSESLL
1			VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAOAPPTFRAO
1 1)		DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
			DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
1 1	1		ACYPEKTTRRMYNLFWRHFRHSEKVIIVNLLLLEARMQAALLYAL RAITRYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEOAAGD
			PEGRRQEPLERRASSASVPAVGASAEGTREDELGSYSGPTSVSR
	1		QRVESLRKKRPLPPWFGLDIGGTLVKLVYFEPKDITAEEEEEE
	1	}	ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
1		ļ	LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCOK
1			LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
	I		FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRD1YGGDYERFG
	1		LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF
		ĺ	SEHEGYFGAVGALLELLKIP

SBO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
J	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ī	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	secuence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
5545	302	131	GAMWSAGRGGAAWPVLLGLLLALLVPGCGAAKTGAELVTCGSVL
1			KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYNRIRG
ì		i	GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
		j	SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVT
			GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
L			DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1		1	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
Į			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
			SLRRHRMHEQQFAHPFLLVLNSFGPHGMHVKLMATMFQNLFPSI
1		ł	NVHKVNLNTIKRCLLIDYNPDSQBLDFRHYSIKVVFVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1		1	AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
			FVSKTEERLQAILBAKBKKLRLKAQRQAQQAQNVQRKQBQREAH
Í	1	1	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
!	1		EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRFGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1 332.	10,52	1	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKVISLKDCVAVAGP
ì			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
	1		SLRRHRMHEOOFAHPPLLVLNSFGPHGMHVKLMATMFONLFPSI
		ļ	NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1	l	l	AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVNFHS
	i		FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
l		ł	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
1			BYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
		L	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5548	1	2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
5548	1 .	2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLV_LLAAYFFRF
5548	1 .	2153	DQTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLVLLLARYFPRF RKQRKAVVSTSDKKMPNGILREQEQQRVMLLSRSPSGPKKYFPI
5548	1 .	2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALKGNETTA DSNETTTTSGPPDPGASCPLLAWLLLPLLLLLLVLLLAAYFFFF REQRKAVVSTSDKKMPNGLURBCEQCYMLLSRSPSGPKKYFPI PVEHLEELIKIRSADDCKOFREERSLPSGHLOGTFELANKEEN
5548		2153	DOTOPPET LAFFFRETMEDLCPLLLVGFSLDFLARALGGNETTA DRNETTTSOPDDGASG_PLLAMILLPLLLLLLV_LLAYFFRF RKQRKAVVSTSDKKMPNGILRBQEQQRVMLLSRSPSGFKKYFPI PVBHLEEEIRJRSADDCKGFREEFNSLPSGHIQGTFELAMKEEN REKNEYPNILENDDSKYLLSQLGFTCSGYJNASYIDGYKRKYK
5548		2153	OOTHOPETIAFFFRATMEDICPLLIVOFSLIPIASALEONETTA DSNETTTISOPDODAGSPILAMILLIPILLILUVALLAYFFRR RKORKAVVSTSDKKMPRGILREDEOGRYMILERSSSOPKKYFPI PVHHLEEE INISADDCKOFPRESTRISSSHIP (IQUI FELANKEEN REKREYPHILPHNHSRVILSQLDGIFCSDVINASVIDGYRKXVS FIAAQOFROTTUNPINAMINGSRATIVMINIALKERKEEKCHOY FIAAQOFROTTUNPINAMINGSRATIVMINIALKERKEEKCHOY
5548		2153	DOTOPPETARTFFERSTWEPLCPLLLVOYSLEINARALGGETTA DOSESTTTSOEDPORASOPLUMLLDELLLLIVLLLAN FERS RKORKAVVSTSDKKOMPNGIJREZEOZ RVMLLSRSPSOPKKYFPI PVEHLEBELRIRADDCKOFFESSFINS JOSH LOGYBKOK RENNEYPHILDMSRVIJSQLDGTPCSDVINS YILDTYKKOK FIJAQDKKQETVNDFWRMVWSQKSATIVNINNLKERKEEKCHQY WPDQCKYTGRIRVCVBCVVLUMTIRKKENCECKHQY
5548		2153	OCTOPPETAFFFERTMEBLCPLLLUGISIPIARALIGISTETA DISTETTISTOPPOGASQPLLANILLULUGISLIPIARALIGISTETA BKORTTTISTOPPOGASQPLLANILLULULULULULULANIPER BKORKAVVSISIKKOMPAN LIRBQBQQZVMLLISSSSSOPKKYTPT VSHILBEER LIRSADDACKOPRESHSIP, SOGII QOT FELLANIKEEN BERNEYPHILPHONSKVIJAGULOT PCSDVIJASS YLODYKEKYK PENAGOPKORTUD PRHAVNOSORATI VUMENIK KERKECKIĞY WEDGGORTYGNI RIVCUBCUVLULUTI RIFFCI DÇILDGOGAVIBA LIVGALIFISTOPRUS PEPET MÜKLÜLKIKVITLINIYADGAVI VI-II-C KOÇLIFISTOPPUS PEPET PÜKLÜLKIKVITLINIYADGAVI VI-II-C
5548		2153	OTHER TAPPER THE LOCAL UNITS THAN ALL MOST T
5548		2153	DOTOPPETAFFFERENBELCELLLUGISSIPJÄÄÄÄLGGISTTÄ DISTETTISSIPPÖRÄSPLÄÄÄLLUGISSIPJÄÄÄÄLGGISTTÄ BISTETTISSIPPÖRÄSPLÄÄÄLLULLULLULLULLULLÄÄÄÄTERF RÄORKAVVISIOKKOMPAI LIRBOROQIVIALLISSIPSOPKIYTYT PVEHLEERILISÄÄDÄCKOPRESTIP, SOOII (100 TELÄNIKEEN REKNEYPHILPHONSKVILSOLIGOTPCSOVIJAASY LOOTYIKKYK PERAGORKOTYON TRIVCUEDCUVLUUTTERFELTOJOLIBOOKAN WEDGOKTYON TRIVCUEDCUVLUUTTERFELTOJOLIBOOKAN UKOGLIPTSIPPÖRUPPTOHUKLEKKYKTINSYPHORDIVING SAGVURTOTFI VILDAMONMEADOKVOVERVAR TRINGROWY TÜROYTFI YOLIALYYLVOOTEJONSI LIKKYLTINSYTTHIPK
5548		2153	OTHER TAPPER THE LOCAL UNITS THAN ALL MOST T
5548		2153	OUTOPETIAFFFERTMEBLEVILLUGISIPTARALIGISISTA DISETTITISPOPORASPILLAMILLULUGISIPTARALIGISISTA BICKTITTISPOPORASPILLAMILLULULULULULULAMIPER BICKRAMVOSISKIMMINALLERDEGOZIVILLISSESSOKKITYPT BICKRAMVOSISKIMMINALLERDEGOZIVILLISSESSOKKITYPT UNBHLEEZILLISJOLOGIFECSIDI INAS ILDOTERGIX BEKNETPHILIPINISHVILSJOLOGIFECSIDI INAS ILDOTERGIX BEKNETPHILIPINISHVILSJOLOGIFECSIDI INAS ILDOTERGIX LIVOLUTINISHVILSJOLOGIFECSIDI INAS ILDOTERGIX LIVOLUTINISHVILSJOLOGIFECSIDI INAS ILDOTERGIX LIVOLUTINISHVILSJOLOGIFECSIDI INAS ILDOTERGIX TIMOLYTTIVALISTINISHVILSTORICHULUNUTERINISHVILSTORICHULULULULULULULULULULULULULULULULULULUL
5548		2153	OCTOPPETAFFFERENBELCHLLUGISTIPARALIGISTITA DENETTITSOPPORASPLLAMILLULUGISTIPARALIGISTITA BENETTITSOPPORASPLLAMILLULULULULULULAAFFFF EKORRAVOSTSOKOMONI LIRBOROGANDELLSSESSOKETTPET PURHLEERI LIRBOROGANDELLSSESSOMI TOPITALISESSES PURHADOROGANDELLSOMI CONTRACTORISESSOMI TOPITALISESSESSOMI PURHADOROGANDELLOMI CONTRACTORISESSOMI TOPITALISESSESSOMI PURHADOROGANDELLOMI CONTRACTORISESSOMI TOPITALISESSESSOMI LUSQUIRTISSOPPORPET COMILICATION PURHADOROGAND LUSQUIRTISSOPPORPET COMILICATION PURHADOROGAND LUSQUIRTISSOPPORPETAFICATION PURHADOROGAND LUSQUIRTISSOMI TORIGINATION PURHADORO
5548		2153	OCTOPPETAFFFERENEL/CHLLUGISTIPARAMIGNISTIA DISTITTISTOPPOGASQHLAMILHALILLULVALAMFERF BKORRAVVSTSIKKMYNGILREQEOQIVMILLISSSSOPKIYTPT BKORRAVVSTSIKKMYNGILREQEOQIVMILLISSSSOPKIYTPT VEHILBEER LIRKSBADACKOPRESENSES DOGII (OT FELLAMEEN REKNETPHILIPANISEVILSQILGGIPCSDVILASSI TOOTYEEKIN PEDAGOPKORTUNDERHAVNOSCHAVI VUMINIA KERENEEKKIYT WPDGGOOTYGNIR IN CURBCUVULUDIT: REFECIO POLBOOCKAV PEDAGOPKORTUNDERHAVNOSCHAVI VUMINIA KERENEEKKIYT WPDGGOOTYGNIR IN CURBCUVULUDIT: REFECIO POLBOOCKAV TEMOVYET YO ALLEYMY MOTELLONS LERKILLTWIGTTHIPA ULISMKROGEYTOY IRAS PIDOTROKTY FILAYGGILAHTVEDN MINIMAKSHITUMITEUMRISHORTUNDIAMIKKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUNDIAMIKEWI (VICTI FOTRE) MINIMAKSHITUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEUMRISHORTUMITEU
5548		2153	OCTOPPETAFFFERTMEBLEVILLUGISTIPARAMIGNISTIA DISTITTISTOPPOGASQILLAMILLULUGISTIPARAMIGNISTIA BINETTTISTOPPOGASQILLAMILLULULULULULAMIPER RIQRAMVOSISDIKOMPROLITROPOGANVILLISSESSOPIXITYET RIQRAMVOSISDIKOMPROLITROPOGANVILLISSESSOPIXITYET PURHLEERILLISHADDUCKUPRESENDIS DE GORITITET PURHLEERILLISHADDUCKUPRESENDIS DE GORITITET PURHLEERILLISHADDUCKUPRESENDIS DE GORITITATION DE REFERENCIA PURHLETHE PURHLET VICTORICULULUS TERPETOPOLITROPEROKUP PURPLICATION DE GORITITATION DE REFERENCIA LINGUIRTSHEPFOVEPTPI OMLKELIKVETLISHVENOFILLISHATTHED KANCHITTITATION DE GORITITATION DE PORTORICULUS DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS PROVINCIA DE LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS LINGUISTIPATORICULUS
			OCHOPPETAFFFERENELCELLUGISIPARAKUGISTYA DISETTYTSOPPOGASQLIAMILHALLILLUGISIPARAKUGISTYA BISTTYTTSOPPOGASQLIAMILHALLILLUGISIPARAKUGISTYA BISTOPPOGASQLIAMILHALLILLUGIAMIPARAKUGISTYA PURHLEER LIRASDOCKOPRESPIS POGII OGI PELLANEEN REKNEYPHILPHONSEVIJAGOLOGI PECSDI YANSI YLOYEKUK PELANGENGENTON PERMINGIGANI YUMITAK REKREEKKIGY MPDGGONTYGNI RUCUBECUVIJUDITI REFETO DOLBOCKANI PELANGENGENTON PERMINGIAMI YUMITAK REKREEKKIGY MPDGGONTYGNI RUCUBECUVIJUDITI REFETO DOLBOCKANI PELANGENGENTON PERMINGIAMI YUMITAK RUCUBECUVIJUDITI RUFARDE YUMITAK KANDARTOTTI YUTAMARAKUGAG, KOVUPER PENGERGENGEN VILSMERGAGYYTO YENS PI DOURGKOY PI ROGELIAH YUDON MILMENENSHI YUMITAKORRODIN PI TUGISTARAKUGITTI YUNITAKORI TERIKANI PENGENGENGENGEN PI TUGISTARAKUGITTI YUNITAKORI TUGISTARAKUGITTI YUNITAKORI PENGENGENGEN PI TUGISTARAKUGITTI AL SINLESYKABGILDVEQOVYKSLELQRHMUQTLEGYESCIKVYO PI DI PENSYMANGILDVEQOVYKSLELQRHMUQTLEGYESCIKVYO
5548 5549	. 915	2153	OCTOPPETAFFFERENEL/CLLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQELAMILALILALILALILALISTE RICKRAWUSISDKOMPHOLIREZEGQENVILLESESSOKKYTPT RECKRAWUSISDKOMPHOLIREZEGQENVILLESESSOKKYTPT PUSHLEER LIKESBODGCOPRESEND SOGIIGOTELAKSEN RESKRIPPHILADINSKYLLSGÖLGIFCSDYLLASSTDOTERGOK PUSHLEER LIKESDDCOPPHOLIREZEGGENGEN SOGIIGOTELAKSEN RESKRIPPHILADINSKYLLSGÖLGIFCSDYLLASSTDOTERGOK RESKRIPPHILADINSKYLLSGÖLGIFCSDYLLASSTDOTELAKSEN RESKRIPPHILADINSKYLLSGÖLGIFCSDYLLASSTDOTELAKSEN LIVSGÜLFTSHEPFUSHKYLTSKYLTGOTELANSTROTELANINGTHED KANGUNGTITTUJARAMANINGLOGVOVEVERVER RESKREPKOMY TIDMOTTFIYGALLSYYLVGOTELDWSLEKKLITHEDTHED KOLLESFERKINVELMENDRICKUTUJANINGKANGUTUT ID DYNR VILISMUSGESTYDI INAST JOGENGOTTFIAL TEABBISHIDLIANUSGOCOGNIND ITTUJGSAGGROTOFIAL
			OCTOPPETAFFFERENELCELLUGISSIPARAMIGNISTIA DISTITTISSIPPORASPLIAMILLULUGISLIPARAMIGNISTIA BISTITTISSIPPORASPLIAMILLULULULULULULAMIPER EKORRAVVISISKIMINAILIRBOROQIVIALISSISSIPSIPRITYSPI PUSHLEERI LIRSADOCKOPRESPISIP SORII OLI TELLAMEEN REKNEYPHILIPIUNISVII.SOLDOI PECSIVII.NAS YLDOYREKIN PEDAGOPROSPINI PERMINNOSCATI VULITIALISEREEKKINY MPDGGONYTON IRVUCEBUVULUTI TIRRETI DILIPEDAGA MPDGGONYTON IRVUCEBUVULUTI TIRRETI DILIPEDAGA MPDGGONYTON IRVUCEBUVULUTI TIRRETI DILIPEDAGA MPDGGONYTON IRVUCEBUVULUTI TIRRETI DILIPEDAGA MPDGGONYTON IRVUTEBUVULULULULULULULULULULULULULULULULULULU
			OCTOPPETAFFFERENELCYLLUGISIPTARALIGISISTA DISETTITISOPPORASPLLAMILLULUGISIPTARALIGISISTA BISTITTISOPPORASPLLAMILLULULULULULULAAFFFF EKORRAVOSISIKKOMPALI REDEGOQIVINLISSES SORKIYTPI PUSHLEERI LISADOLOCYPERESISTA DORULUGISISSES SORKIYTPI PUSHLEERI LISADOLOCYPERESISTA DORULUGISISSES SORKIYTPI PUSHLEERI LISADOLOCYPERESISTA DORULUKSI LOTOPEROXI REKNET POSILAMINISTA LISADOLOCYPERISTA SORKIYANI LIVOLUHTINISTA LISADOLOCYPERISTA LISASI TODYEROXI LIVOLUHTINISTA LISADOLOCYPERISTA LISASI SORKIYANI LIVOLUHTINISTA LISADOLOCYPERISTA LISASI SORKIYANI LIVOLUHTINISTA LISADOLOCYPERISTA LISASI SORKIYANI LIVOLUHTINISTA LISADOLOCYPERISTA
			DOTOFPETAFFFERMELCELLUGISTIFARALIGISTETA DOSETTITISTOPPORASPLLAMILLULUGISTIFARALIGISTETA BENETTITISTOPPORASPLLAMILLULULULULULLULAMIPER EKORRAVOSTSICKOMONI LIRBOROGANMILLISSESSOPKITTET EKORRAVOSTSICKOMONI LIRBOROGANMILLISSESSOPKITTET PURLIEREI LIRBOROGANDERIS DE SOBILIOTETELLIAREER PURLIEREI LIRBOROGANDERIS DE SOBILIOTETELLIAREER PURLIEREI LIRBOROGANDERIS DE SOBILIOTETELLIAREER LIRBOROGANDERIS DE VORDENIULULULULULULULULULULULULULULULULULULUL
5549	. 915	256	OWTO PET LAFT PROTING LOCAL UNGSET PLANALISMS TAR AND SENTITIVES POPOLOGO PLANALISMS LOCAL LAFT PROTING AND SENTITIVES POPOLOGO PLANALISMS LOCAL LAFT PE EKORANVOSISKIMONALI REDEOQUIVALISMS SEGURINI PET PURHLERE ILE RISADOCKOP RESERVES POR UNIONI PETALANEZH PETALANCEZH P
			OCTOPPETAFFFERTMEBLEVILLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQULAMILLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQULAMILLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQULAMILLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQULAMILLUGISTIPARALIGISTETA BORSTITTISTOPPOGASQULAMILLUGISTIPARALIGISTIPARA
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5549	. 915	256	DOTOPPETAFFFERMELEVILLUGISIPTARAKUGISTTA DOSETTITUSPOPOGASQULAMULAULULULULULATIPTARAKUGISTTA BEKETTTISPOPOGASQULAMULAULULULULULATIPTE BEKORRAVUSISISIKOMPAOLI URBORQQINVILLISSES SESOPETITYET BEKORRAVUSISISIKOMPAOLI URBORQONIVILLISSES SESOPETITYET BEKORRAVUSISISIKOMPAOLI URBORQONIVILLISSES SESOPETITYET BEKORRAVUSISIKOMPAOLI URBORQONIVILLISSES SESOPETITYET BEKORRAVUSISIKOMPAOLI URBORQONIVILLISSES SESOPETITYET BEKORRAVUSISIKOMPAOLI URBORQONIVILLISSES SESOPETITYET LUSQUALITYSHOPPOUPETY URBORQONIVILLISSES SESOPETITYET LUSQUALITYSHOPPOUPETY URBORQONIVILLISSES SESOPETITYET LUSAVUSITYET SESOPETITYET SESOPETITYET SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE SESOPETITYET LUSQUALITYSHOPPOUPETY SERVICE LUSQUALITYSHOPPOUPETY SERVICE LUSQUALITYSHOPPOUPETY LUSQUALITY LUSQUA
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5549	. 915	256	DOTOPPETAFFFERMEBLEVILLUGISIPJARAKUGISTYA DOSETTYTOSPODAGSPLLAMUHALHALILULUGIAAFFFF RECREAVUSISIRKOMPANILERDEGGGNYMLESSESDEKTYST RECREAVUSISIRKOMPANILERDEGGGNYMLESSESDEKTYST RECREAVUSISIRKOMPANILERDEGGGNYMLESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESSESDEKTYST LIVERGGNYMLESSESSESDEKTYST RECREATIONSEVILLEGGGNYMLESSESSESSESSESSESSESSESSESSESSESSESSESS
5549 5550	915	256	OOTOPPETAFFFERTMEBLEVILLUGISIPJAARALGGISTTA DESETTTISPPOTAGSQLIAMILLUGISIPJAARALGGISTTA BESTETTTISPPOTAGSQLIAMILLUGISIPJAARALGGISTTA BESTETTTISPPOTAGSQLIAMILLUGILLUGISIPJAARALGGISTTA BEKORTPPOTAGPOTAGSQLIAMILLUGILLUGISIPJAARALGGISTTA BEKORTPPOTAGPOTAGATAGATAGATAGATAGATAGATAGATAGATAGATAG
5549	. 915	256	DOTOFPETAFFFERMELCELLUGISTIFARALIGISTITA DOSTETTITOSPOCASQULAMULALULLULUGISTIFARALIGISTITA DISTETTITOSPOCASQULAMULALULLULUGISTIFARALIGISTITA BENETITASPOPOCASQULAMULALULLULLULAMUSER PROPERTY ENCREAVUSTESICHOMORIULEROROGINGLISS SPROPERTYPET PURALOROGINGLISSICATORIUS SPROPERTY PURALOROGINGLISSICATORIUS SPROPERTY PURALOROGINGLISSICATORIUS SPROPERTY PURALOROGINGLISSICATORIUS SPROPERTY PURALOROGINGLISSICATORIUS SPROPERTY LUSQUIRTSHPPOTOFPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPPOTOFPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELIKUTELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELISVYANOGEVUS LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMIKELISVE LUSQUIRTSHPOTORIUS SPROPETOMICH SPROPETOMICH LUSQUIRTSHPOTORIUS SPROPETOMICH SPROPETOMICH LUSQUIRTSHPOTORIUS SPROPETOMICH SPROPETOMICH LUSQUIRTSHPOTORIUS SPROPETOMICH SPROPETOMICH LUSQUIRTSHPOTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH SPROPETOMICH LUCAMICOVICTORIUS SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOMICH SPROPETOM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			WFVFRRYAEFDKLYNTLKKOFPAMALKIPAKRIFGDNFDPDFIK
1)	Į.	QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
		(DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
1	l .	Į.	LLAKRKLDGKFYAVKVLCKKIVLNRKEQKHIMAERNVLLKNVKH
		Į.	PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
}		l	FYAAEIASALGYLHSIKIVYRDLKPHNILLDSVGHVVLTDFGLC
		ļ	KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
1	i	1	BMLYGLPPFYCRDVARMYDNILHKPLSLRPGVSLTAWSILEELL
			EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV
1	ì		AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
5552	2748		FSYAPPSEDLFL
5552	2/48	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
1			SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKKEKEKHL
1	1		DDEERRKRKEEKKRKREREHCDT3GEADDFDPGKKVEVEPPPDR
1			PVRACRTQPAENESTPIQQLLEHFLRQLQRKOPHGFFAFPVTDA
1	1		IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
1			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
1	(EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAEEHVL
1			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
1	(ALSMQNMSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
j	J		GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDJAKVG
1	(DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
	1		HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL
1	(GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPPHVVTPLLESWALSQVAGMP
1			VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
1	}		AAAYAARKIGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
			EANLRAGELAKROGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1	}		PGALVLAVGGGGLLAGVVAGLLEVGWOHVPIIAMETHGAHCFNA
i i	ļ.		AITAGKLVTLPDITSVAKSLGAKTVAARALECMOVCKIHSEVVE
			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLOAEGCL
			PPSLTSVVVIVCGGMNINSRELQALKTHLGQV
5554	166	2318	CSGRTGGRGSLRPARNVCLTCKLSGAETRGLLCPALRTWIMKVL
1 '			GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
1 1	1		WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ
			VHTFEIFQKELNESENSVFQAVYGLQRALQGDYKDVVNMKESSR
	}		QRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSML
			DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEBE
1 1			ANSKONITKREVEDDLGLSMLIDSONNOYILTKPRDSTIPRADH
			HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
			SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
1			YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLCMLVTQDVQLGLFMAVMPTLIOAGAS
			ASSSIVVEVERILVLIGQILFSLAAVFLECTVIKKYLIGFYYRK
1			LHMBSKGNKBILILGISAPIFLMLTVTELLDVSMELGCFLAGAL
1 1			VSSQSPVVTREIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
1 1		J	TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
1 1	1		SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLNRAAI
1			TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR
1 1			GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK
1			KAYRKLALQLHPDRNPDDFQAQEKFQDLGAAYEVLSDSEKRKQY
1 1)	ļ	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
1 1		i	GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCROE
1 1	1	ļ	MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
I			GMEYPFIGEGEPHVDG3PGDLRFRIKVVKHPIFERRGDDLYTNV
1 1		ļ	TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
1 1			PNFONNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGŞVQK
			VYNGLQGY
5556	5835	3346	RTRGMSKNCVPMBFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1	1	LRELDESYTEKFTÖFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
	1		YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
			DALVLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
			QSLEVVARVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
	i		FNDALTVVERLVKVTLYGSCIKLYNIKTAVPSVLKPDLIDVHAQ
	1		SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
			KVODKLLLSACHLLVSLATTVRPVFLISIPAVOKVFNRITDASA
	i		LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
	ł		SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
			SGESTKSRQICYQSLQESVÇVSLALFPAFIHQSDVTDEMLSFFL
			TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
	l		VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
)		PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
			QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
	i		TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
	ļ		AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
			RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLEDKDMWIPVVGLPRELELSALAGAGEFCILGSEAATE
	l	1	KHLPARNHCGLSDSSPQLWPEPDFRNPFRKASKASLDFKRYVTD
	}]	RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV
			ALESDKTFIPHLRSLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
	1		AMSSRGLFKNIGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
		1	WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
			LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
		i	LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
	l	ł	KWLYDETLEDR
5558	1509	96	RAGCTHPOVPADLGAPAEPRRPOKTCVCLLQPOPGGORGPTTMI
			TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
	Í	Ĭ	LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
	Į.		YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
			LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
			GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
	1	ł	SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
		}	CPMLKRFARMIBQRAVDTSLYILPKEDRESLQMAVGPFLHILES
	i		NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
		i	FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
5559	150	1983	LNAMSVYTLSPEXYHALCSQTQVMEVGNEE
2559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
		(ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK LMOREMSMDESKOVETKTDAKNGEERGRDASKKALGPRRDSDLG
		1	
		ļ	KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
		}	VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
į			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE MEWAKKEDDEKVKGERRRITDTRKEGERMKRAAGNTDMKKEDEK VRROTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG PTKPSEGPAKVEEKAAPSIFDEPLERVKNNDPEMETSVAVNNSDC
			UDKRAGKOGRGERRAVATKREESEKGSDRYTGLSDKUKKRSE KEVAKKEDDEKVKGERRITTTTKEGEKKKRAGGNTDMKKEDEK VKROTGNTDTKKDDEKVKNEPLLEKRAGDDSTKTFERGTPSG ETKPSGOPAKVSEBAAPSIFDEPLERVKNDPERTENNINSDC TINGILVRIFEALSENTVKLGELAUTRADEVAFAIATUKAN
			UDKKLAGKOGRGEBRAVATKKEEKKGGENNTGLSJRDKUKKREE MKEVAKKEDEKVKGERRITOTREGENKRAGGNTÜKKEDEK VKRGTGNTOTTKKDDEKVKRABPLEBERAKUDKKTEPEKGPENG PTKPSGOPAKVEBRAADSIDDELBEVANDDEKTENVINISDC TINEILURFTEALEPNTVVKLFALANTRADENVAFIAIAIMLKAN KTITSLKUBSHITTKKGILAIFRALLONNTLIELRFHOORHICG
			VOKEMACKOR GEBENAVATKEEEEKKOS DENTVIJAS DODIKKERSE KKRAS DENTVIJAS DODIKKERSE KKRAS DENTVIJAS DODIKKERSE VARDOTORITOTIKKODEKVIKASEPLAIEKKADADOS YTT. DE EKOP PROPERDE PARA PARA TIDER DENTVIJAS DENT
			UDEKRAAKUOROKERAVITKKEESKKOGERIVIJASOKUKKESE KREVAKKEDOKYKKEREINTITAKEESKKOGERIVIJASOKUKKESE VRAGTORITUTKKODEKVIKKISPLIEKENAUDDSKITTSEKOTPOK PEROPORITUTKKODEKVIKKISPLIEKENAUDDSKITTSEKOTPOK PEROPORITUTKKODEKVIKKISPLIEKENAUDDSKITTSEKOTINISD LITHELUKRYTEALEPHTYVELFALANITADDEWAFATA IMILKAN KITISIALIDSHITTIGISTILLI REPULLORITUTELEFINORITCO OKTEMETAKLIKRITTILLIKUKYHPHAGAPHATYTTILLISHINING OKKILOROKOROKAGEKELUKLIKYHPHAGAPHATYTTILLISHINING OKKILOROKOROKAGEKEKULEKYPYAGAVAKAGSYKSESOMSEK BESHKISSKKOGAPAAPPPPPPPAPALISHILLISHIJAPATORIM OKVILADRIKKHSROQLIALATISSKILOKIKKYEVEKILOKIKKOP
\$560	9	921	UPKENACKOPROBERANTKEREEKKOSURNITULASURUKKETEK KREVAKKEDDEKVIRGEREITUTAKEBEKKOSURUTULASURUKKETEK VKROTORITUTKKODEKVIKAIRILAEKENADOSKITUTEKOOPEN VKROTORITUTKKODEKVIKAIRILAEKENADOSKITUTEKOOPEN VKROTORITUTKKODEKVIKAIRILAEKENADOSKITUTEKOOPEN VKROTORITUTKKODEKVIKAIRILAEKENADOSKITUTEKOOPEN VKROTORITUTKOOPEN VKROTORITUTKUTALIAATILAEVIKAIRILAEKEN VKROTORITUTKOOTEN KONTORIORITUTKOOTEN KONTORIORIORITUTKOOTEN KONTORIORIORIORIORIORIORIORIORIORIORIORIORIO
\$560	9	921	UDKEMAAKOGRERAVITKKEESKKOGERIVIJAGODKKERJEK KREVAKKEDDEKVIKGERRITUTKEEDEKKAGERIVIJAGODKKERJEK VRROTRITUTKKODEKVIKKISPLIJEKENAKODSKITCESEKOTEGE VRROTRITUTKKODEKVIKKISPLIJEKENAKODSKITCESEKOTEGE VRROTRITUTKKODEKVIKKISPLIJEKENAKODERIVETKOVINISDO LITKETLUKPETEALEFITYVILFALANITEADDEWAFATATIMIKAN KITISIALIDABHITGAGI LIA FERLALORITUTLIJEKSHONIKO OKKILOROKODARAGEKEKLULEKYPEHAGAVRAGSYESEJOSEK PSEKRISKIKGGAPAAPPPPPPPIAPPLINISHLINISLISATIORN OKKILOROKODARAGEKEKLULEKYPEHAGAVRAGSYESEJOSEK SEKVEPÄALSVÄNGLISHSSOLGKEVEVEVILGESTIGABECVAN SSVEPÄALSVÄNGLISHSSOLGKEVEVEVILGESTIGABECVAN
5560	9	921	UDKINAAKUOROKERAVAYKKEESKKOSURVITULASUOKKKESK KREVAKKEUDEKVIKSKERHITURKEEDEK VAROTOKITUTKKUDEKVIKAISPLIEKEAJUDSSTITUSEKOTPOS VIKROTOKITUTKKUDEKVIKAISPLIEKEAJUDSSTITUSEKOTPOS TITNBELUKRITEALESHITYVELEALANTEAJUSVATA IA MILKAN KITTISTALIDANITITUSGI LIAL ERIKULOKNITUTELEIDANITIKOKITUG OKTOBELAKLIJKOSITULIKUOTHITALARITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKUOTHITALARITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALARITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALARITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALARITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALORITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALORITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALORITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALORITYTUTKILISKININKO OKTOBELAKLIJKOSITULIKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYTIINKOOTHITALORITYINKOOTHITAANINKOOTHITALORITYINKOOTHITAANINKOOTHITAANINKOOTHITAANINKOOTHITAANINKOOTHITAANINKOOTHITAANINKOOTHITAA
\$560	9	921	UDKEMAAKOORGERAVITKKEESKKOGERIVIJASOKKKESE KREVAKKEDOKKKEREITUTKEEBEKKOGERIVIJASOKKKESE VRROTORITIKKODEKVIKSIBPLIEKENAKOOSKITTEEROTPEG PREPORDARVEKRARAPITEDELEKENAKOOSKITTEEROTPEG TETRORITORITORITORITORITORITORITORITORITOR
5560	9	921	UDKEMAAKUORGERAVATKKEESKKOSURVITULASUOKKKAS KREVAKKEDDEKVIKSIRRIPITUTEKSEEKKOSURVITULASUOKKEESK VARGTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES VARGTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES VIKROTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES LITNELUVRITEALEPHTYVELPALANTERAJUSKATA LIMILAN KITTISLIMLOSIMITUSTOSI LIA FERNIKALOSINITUSELEPHORETI CO GOKTOBELAKILIKENTITUKUGHERIAGUPRYTUTHLISHININIK GOKHLOOFROMEAKOEKULIKUS PERGAVKASI SEKSEDJESK LESPIKOSIKOSU DAAPPIPPIPILIPI. LIVELIKISLISTATIOKO LOSKI USEKSENIKA SANGARI GOOD PILILASI TAJEKEVINI CORI IGE TVARMUVELIKUTKESTOESEDLIRAGISTUTKISSED SIVUPERALUSKOSKOLISPAGILIKASIKI CARALHARIOKSI PEPPEKKOPILASII LIUVROMITUSEKSI KI CARALHARIOKSI PEPPEKKOPILASII LIUVROMITUSEKSI KI CARALHARIOKSI PEUROLIVANIKA CARALHARI
\$560	9	921	UDKEMAAKUORGERIAVATKEEEEKKOS DENTULASDOMIKERSE KKRISTERITULASDOMIKERSE KKRISTERITULASDOMIKERSE KKRISTERITULASDOMIKERSE KKRISTERITULASDOMIKERSE KKRISTERITULASDOMIKERSE KKRISTERITULASDOMIKERSE KRISTERITURS KRISTERIT
5560	9 2175	921	UDKEMAAKUORGERAVATKKEESKKOSURVITULASUOKKKAS KREVAKKEDDEKVIKSIRRIPITUTEKSEEKKOSURVITULASUOKKEESK VARGTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES VARGTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES VIKROTORTUTKKUDEKVIKSIBPLIEKERAJUDSKTITUSEKOTPES LITNELUVRITEALEPHTYVELPALANTERAJUSKATA LIMILAN KITTISLIMLOSIMITUSTOSI LIA FERNIKALOSINITUSELEPHORETI CO GOKTOBELAKILIKENTITUKUGHERIAGUPRYTUTHLISHININIK GOKHLOOFROMEAKOEKULIKUS PERGAVKASI SEKSEDJESK LESPIKOSIKOSU DAAPPIPPIPILIPI. LIVELIKISLISTATIOKO LOSKI USEKSENIKA SANGARI GOOD PILILASI TAJEKEVINI CORI IGE TVARMUVELIKUTKESTOESEDLIRAGISTUTKISSED SIVUPERALUSKOSKOLISPAGILIKASIKI CARALHARIOKSI PEPPEKKOPILASII LIUVROMITUSEKSI KI CARALHARIOKSI PEPPEKKOPILASII LIUVROMITUSEKSI KI CARALHARIOKSI PEUROLIVANIKA CARALHARI

Deginning Deginning Decation Cocation Contemporaling Cocation Corresponding Co	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not Inuclectide Iocation Iocation Iocation Iocation Inuclectide Incident			nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
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TEHLEVUOTEINNETYGASSAAPKETAGUTEVKUPPUUSHTADEPU SESSEMPUTAINNET ISRAAPKOULANGGARTHOTEVKUPPUUSHTADEPU SESSEMPUTAINNET ISRAAPKOULANGGARTHOTEVANSAGETLA TTUQHINIALGARTHOTEVSEVPENA TTUQHINIALGARTHOSUSTYUPPUN TTUQHINIALGARTHOSUSTYUPPUN TTUQHINIALGARTHOSUSTYUPPUN TTUQHINIALGARTHOSUSTYUPPUN ALKOTINIALGARTHOSUSTYUPPUN ALKOTINIALGARTHOSUSTYUPPUN ALKOTINIALGARTHOSUSTYUPPUN KAHABBISHALGUSISHI ILLEFARAALMIKISHIFETYELISHI SEALEHDESVUJAGGELAQKILGURVENYXYRQUEETTELISHIS TAAGKAUGOTSHALGISTINIELDEVUDHEGSPALIPSTIPHLE PHULLAPLUSSRTLESTINIALGARTHLIPPUNGSI ELIVSSINIEL VOOGILGSGUSVESIILQUITPUNGSITLIPPUNGSI ELIVSSINIEL VOOGILGSGUSVESIILQUITPUNGSTILLIPPUNGSI ELIVSSINIEL VOOGILGSGUSVESIILQUITPUNGSTILLIPPUNGSI ELIVSSINIEL VOOGILGSGUSVESIILQUITPUNGSTILLIPPUNGSI ELIVSSINIEL				
SBSBMP/OTAMYP.RESAFROGMINAGGAYYTGPYZAAQBHYIHE TYTVOQPASIS PALTPANVAAPERIOAMINAGGAYTTGPYZAAQBHYIHE TYTVOQPASIS PALTPANVAAPERIOAMISAAGTL TYTOQTALGARUVSKPYTAAQOTDAYS YVEPIN TYTOQTALGARUVSKPYTAAQOTDAYS YVEPIN ENGLOF 1GSTLDFIANGESTRAFIJALUVOKLEPAGEROLDERSOTYAG ANOTONISGIJAADDA TAAGOTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAA				
TTVVQPNSIPS-ALTPANVAAPETROVANONTAGTTMANSACTLI 5582 5775 2739 TITURGHALDENSVERVENTVASTVEPHN ENGLIGHT STATEMENT STAT				SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAOPHVTHH
TTOGETALGARPUSMPTURAGOTDATSTUPPIN TITHRINNIT INTUITAMINGSAGAMERESSAFALBERGERKADT REGIGATGSTTLPLKGRETKAFLLKUNDILPAGERDLERECKEADT REGIGATGSTTLPLKGRETKAFLLKUNDILPAGERDLERECKEAD AUGUTINGSUNDATARSDOVALPERLECKLELVERECKETTEIGLY KRALADSBRALGLISSES IRLERRAGIAERIGHERATSTSSRG KRALADSBRALGLISSES IRLERRAGIAERIGHERATSTSSRG TAAGTALOGTSRAGLISSISTICHEROTUPPUNGGSRLLUGT PHALALADLESSRTLGETTSILDDPSQDOVROPELDTILLSISSI VOGGISGGSUNSERLUGTLEPPROSTILLPPVISSISTES	1			TTVVQPNSIPSAIYPAPVAAPRTNGVANGNVAGTTMAMSAGTLL
5582 5775 1TIRININVITEURIANIGGSAGARGERSIAFELDERGERADI REGLOFICATE PLAGERINA PLAGUNOLAGAGERSIAFELDERGERADI REGLOFICATE PLAGERINA PLAGUNOLAGAGERIANIGE PREPADVA ALOOPINGUNIADIVAASOVALDERGLOFICATE PLAGUNOLAGAGERIAGAGERIA PLAGUNOLAGAGERIA		0		
ALOVINGIAN/ADVAASDVALPEELLCKLAVREAACYFYEGJY. KKALAGBISKALGUBSSI ILALEFRAALAKIGSHERLAYCGSRC SLALENDSVYLGGGLAGAKLGUSVEAYAYRQELEFFELLSIG. TAAGVAQOTSHAGASIGJOTEFFEVODEGSPALLOFFFIPLE PHULLAFLESSRFLESTIGLADPSDQDVFSEELDFLLSIGS. VQGGLGSGSVESELDGLIVEPFOOTELLSPYSGSLEY VGGGLGSGSVESELDGLIVEPFOOTELLSPYSGSLEY VGGGLGSGSTEN VGGGLGSGSVESELDGLIVEPFOOTELLSPYSGSTEN VGGGLGSGSVESELDGLIVEPFOOTELLSPYSGSTEN VGGGLGSGSVESELDGLIVEPFOOTELLSPYSGSTEN VGGGLGSGSTEN VGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5582	5775	2739	
KKALADSKAIGLUSESI IRLEFRIRALAINIGSHERAYTGCSSRC SLALEHDESYTLOGGEAGULGUVRAYTEPGELTSFGLLSHG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTFINPLF PHILLIAFILESSKTLEFTDSLIDDFSDGDYTGELDTLLISTSIJ VQGGISGGGVESELDGVITLEPFVGSSIPTELPFVGSSIPTE				
KKALADSKAIGLUSESI IRLEFRIRALAINIGSHERAYTGCSSRC SLALEHDESYTLOGGEAGULGUVRAYTEPGELTSFGLLSHG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTFINPLF PHILLIAFILESSKTLEFTDSLIDDFSDGDYTGELDTLLISTSIJ VQGGISGGGVESELDGVITLEPFVGSSIPTELPFVGSSIPTE	1			ALVQYMEGLNVADYAASDQVALPRELLCKLEVNRAACYFTMGLY
SLALPHDESVYOLGGBLAGKLGLBVRKAYKERGELETFSLLSKU TAMGVAUGTSKANLGSLDIBETTOVUPBRESSFALLEFTFINELF PHULILAPLESSFALPSTOSLDOPSUGVEGELDTLESSEL VOGBLESGEVERSELDGLEVFOGTFELEFVEGSES FLYSSPJPF]			EKALEDSEKALGLDSES IRALFRKARALNELGRHKEAYECSSRC
PHVLDLLAPLDSSRTLPSTDSLDDPSDGDVFGPBLDTLLDSLSL VQGGLSGSGVPSELPQL1PVPPGGTPLLPPVVGGS1PVSSPLPP	1 1	Í	ĺ	SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1 1	1	Į.	
			ļ	
ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL	1 1	1	i	
				ASPGEVALPSKALMANSVEHALDPPGPTLDPLDLLPYSETRLDAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
í	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide delstion,
	sequence		\=possible nucleotide insertion)
1	1		DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
1	J		TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
4	1		RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
1			KYGDNCTFAYHQBEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT
1			IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
1	1		HSFYNNKCLVHIVRSTSLKYSKIRQFQBHFQFDVCRHEVRYGCL
i	i		REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
1	[AGKASSSNGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPOOYD
1	l		LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMXENKILDMOCTY
	1		DMWLKKHNPGKPGEGTPISSREGEKQICMPTDYADIMMGYHCWL
1	1		CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
1			LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
	1		KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCROGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
			IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
1			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
	i		HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
1			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
			SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
1			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1			LVITSKAGEVIKHGDLRCVRDEGNPIYKAPLEKGILIIQFLVIF
			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
5584	3	1265	WROHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDLLGVKPSASPEE
0501		1205	IKKAYRKLALKYHPDKNPDEGEKFKLISOAYEVLSDPKKRDVYD
Í			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
1			HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGXKGSVEKCPL
			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
1			SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
J			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1	i i		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1			PEKHWLSLEKLPQLEALLPPRQKVRICDDMDQVELKEFCPNEQN
5585	2619	915	WRQHREAYEBDEDGFQAGVQCQTA LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
		540	YHSLTYATILEMQAMMTFDPQDILLAGNMMKBACMLCQRHRRKS
1 .	J		SVTDSFSSLVNRPTLGQFTEREJHAEVCYAKCLLQRAALTFLQD
1	1		ENMVSFIK3GIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
			GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR
			YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
			CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
			RRYFSSNPISLPVPALEMMY:WNGYAVIGKQPKLTDGILEIITK
1			AEEMLEKGPENEYSVODECLVKLLKGLCLKYLGRVQBAEENFRS
(1		ISANBKKIKYDHYLIPNALLELALLLNEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
		222	YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCORHRRKS
1		l	SVTDSFSSLVNRFTLGQFTEBE HAEVCYAKCLLQRAALTFLQD
		i	ENMVSF1KGG1KVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1 1		ľ	VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLOLEEGAS
			GHSPRSVLCVMLLLCYHTFLTPVLGTGNVNIEEAEKLLKPYLNR
1 1	1	1	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
)		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
1 1	ì		RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
]]	1	J	AERMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
	í	1	TSANEKKIKYDHYLIPNALLELALLIMEQDRNERAIKLLESAKQ
5587	1768	148	NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL SSAVPDGAVGRPVAVAVGGPFHSCRCRPCCIMAAIGVHLGCTSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T-Threonine, V-Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	Bequence	\=possible nucleotide insertion)
	Bequence		
1			CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
1	}		RNISHTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
1	i	1	IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
1		l	DFGEKQKNALGEAARAAGPNVLRLIHEPSAALLAYGIGQDSPTG
1		l	KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
		1	TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
!	1	l	ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
i			NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
l .		l	VIPIGAAIBAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
1			SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
	1	!	EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
1	1	j	GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
i .	1	ł	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
			VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
1	1	[AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
		l	RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
ì		}	PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
		!	GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
Ì		İ	ATLGAAGQPLGGESICSARAPAKYSITFTGKWSCTAPPKOYPLF
	ļ.		RPPAOWSSLIGAAHSSDYSMWRKNOYVSNGLRDFARRGRAWALM
			KEIBAAGBALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
ì			VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF
			TFSSPNFATIPODTVTEITSSSPSHPANSFYYPRLKALPPIARV
İ			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
	J		SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
			DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVCRGSGDFDDFNL
		***	EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
1	1		LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
Į.			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKFDKG
1			KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
ł		1	QQKKPCFSIQQGLNADYVKGENLEAVVCREPQVKYSTLHTOSAE
1			PPPPPBPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEBEAMA
3332		1171	LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
l			DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVFMLV
l			PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
l			
			CAPAREDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
	1		RQLEEBQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET
1	i		MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI
	ł		GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
1	1		KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
			ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
5592			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
	1		VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1	j		TAGQEDTIOREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
			IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
] [ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
			MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
			SSGIVADLSEQSLEDGEERGEEDPEEEHELPVDMETINLDRDAE
1 1			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
			BEDLYDNQIKKIENLEALTELBIEDISFNLLRNIEGVDKLTRLK
1	i		KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIBGLQNLVNLR
			BLYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
			EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
NO:			Glutamic Acid, F=Phenylalanine, G=Slycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	podmonoc		MDALPSVROIDATFVRF
5594	3	1113	
5594	3	1113	HASGGRAANMAABRGAGQQQSQKMMEVDRRVESBESGDEEGKKH
1		ł	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1		i	DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
1	1	ſ	ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
1		ł	KLFLVNNKISKIENLSNLHOLOMLELGSNRIRAIENIDTLTNLE
1			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1		1	ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1	ļ		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLOKDPOYRRKV
1			
FF0F	I		MLALPSVRQIDATFVRF
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1	1		PIALANSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
1	l	l	LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1	l		AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
1			NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
1	l		NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSOTHRAFGD
1			VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
1			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1			IALGEPLYRVSTGNYEYRLILRCROEARARFSOMRKDVLEKMEL
I			LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
1	ì		
1 .	1		HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
			GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
1			FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
1			KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTI/PHVRYPAGDLSGHLLAYLSLSP
1 1			VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIOEPR
1 1			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHOTNNA
1			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
í I			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FEYTVTRAEARNRORKLGTKLO
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1 3330	1 220	2440	
1			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
			DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRNMSQLELLSGG
			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTWNTECGKLLEE
]]			IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVOSGIKGGDERGLL
1			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1 1			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
]			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1 1			
	1		TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1 1	l l		SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
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1 1			VPLLGSGVPPHPPAPSPCCSGOTMLKMLSFKLLLLAVALGFFEG
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1 1			EMLCGGFYPRLSCCLRSDSPGLGRLENK: FSVTNNTECGKLLEE
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1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
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1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1 1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
į 1			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1 1			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPD3FLYIILGDGM
1 1			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
, !	J		TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

Deginning No: Household				
Mo: moleocide location corresponding	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortisponding				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequ	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence Segrine, TwThreonine, V-Vallane, Segrine, TwThreonine, V-Vallane, Segrine, TwThreonine, V-Vallane, Segrine, TwThreonine, V-Vallane, Segrine, TwThreonine, V-Vallane, Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence SEQUENCE SEQ				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence sequen				B-Droline, M-Methionine, N-Asparagine,
residue of anino acid sequence ##TYPytoplan, Y-Tyrosine, X-Unknown, **stop Codon, /*possible nucleotide deletion, V-possible nucleotide insertion) ### APP				F=Proline, Q=Glutamine, R=Arginine,
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				GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	A-Alstidine, I=ISOledcine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
			Q
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
1	i	l	RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
1		i	TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
			ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
			SKPKTETCSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
		!	SQSQVIGTEGGKNASTSATSRSYSSIILPVVTALIVITLSVFVL
	i		VGLYRMCWKADPGTPENGNDOPOSDKESVKLLTVKTTSHESGEH
			SAQGKTKN
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	l .		SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1			IVYKDMVTKMQQBITFQQVMSQIANVKKDMIILEKSEFSALRAE
	l		NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
			EKKLLELRTEIVALHAQQDRALTCTDRKIETEVAGLKIMLESHK
	l .		LDNIKYLAGSIFTCLTVALGFYRIWI
5625	1	1180	TIPSSAMAGRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
			AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
			TAPDRATAVATASRLGPYVLL3PBEGGRAYQALHCPT3TEYTCR
			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAPFTRTH
1			GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
i			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
1			ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
	l		RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ
			DPMPLAPTRSELWEAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVONPATST
	02	2021	
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTCRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLTNLRKGYLPNYNLVQFLGFSWIFVN
i l			LTVRPCILGKESPYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLEGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			TEDVODUM CONDENSIT OUT DUTT WITH AND A SECOND
			IFRYSPYMLTCIDMDWKVLTWLRYTLWiPLYPLGCLAEAVSVIQ
1	i		SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
5627	3123	2011	RHLYKQRRRRYGQKKKKIH
3027	3423	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1 1			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1 1			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLINLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCTLGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1 1			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
1			"FRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
5628	75		RHLYKQRRRRYGQKKKKIH
3020	/5	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
1			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
) 1			GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLBSR
1 }			TREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
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1 1			LEAQVESLKERLLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
	ļ		DLNRVLBENRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
1 1			QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
1 1	I		SSQLAQMQCMITNVEAQLABIRADLERQNQKYQVLLDVRARLEC:
1	1		BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
			ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRN/LRERAGLSSAAVQTRIGNSAASRRSPAARPPV
	1		PAPPALPRGRPGTBGSTSLSAPAVLVVAVAVVVVVVVSAVAWAMA
1	1		NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
1 1	I		QEVILQLFIDGIINKLIGCYVGNINEDVVLVRIYGNKIELLVDR
	I		DBEVKSFRVLQAHGCAPQLYCTFNNGLCYFFIQGEALDPKHVCN
			FAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKNGKYFSLIPTGF

SEQ Predicted Predicted end Inclo ecid segment containing signal Incloudide Incloudi	cid, E= ycine, e, *=Stop
No. nucleotide location location corresponding cor	ycine, me, *=Stop
corresponding to first amino acid	*=Stop
to first amino acid residue of residue of residue of amino acid am	*=Stop
amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Vallne, V-Vallne, amino acid sequence S-Serine, T-Threonine, X-Unknown, Codon, /-possible nucleotide deletic possible nucleotide deletic LCKMI YEEGODVG-IDETSONILABETPHICELISTICS LCKMI YEEGODVG-IDETSONILABETPHICELISTICS UNDEALSEPHICAMALIQAKYSTIEFDELGYAIVRE SVENALUSE S-VENALU	*=Stop
residue of amino acid anino acid sequence (Codon, / Npossible mucleotide deltric pequence) ### Application	*=Stop
axino acid sequence Codon, /=possible nucleotide deletic	*=Stop
ocquence Vepossible mucleotide insertion ADBININEPISFISFSIDESFYMERISHSISS LCKNI IYEEQOSUVOPI DVEYGYMYLAIDIGHIPP DYSIVPORELOGOMERATILENPERGEOTISTICS NOFALASEFFWILMALIQAKYSTIEFDFLGYTAIVRE EVPLAKVOE EVPLAKVOE	
ADEDLYKEPT-BOTESSOJIOGENTWKEBILSKLASS LCKMI IVERKOODVOFI DIEKSCHVILAVIOLISKIF DISLIPDELOSOMLRATLERSPERSOTEUTEKE NOPALASKEPRIGLIAALIQAKYSTIEFDELGYAIVRE BYDALKVOE	
Leriiiyee(aguvgidyee(sinilaydiam); Diskufderlagomlanilayakefegotevtek Nopalashepmajmaliqakystibeddelayive Bevalkye	WILL CHINDS
Dyslyddriosomeryleaukeprofotevieke Nofalashffwgimaliqakystiefdfigyalvre Evyalkybe	
NQFALASHPFWGLWALIQAKYSTIEFDFLGYAIVRE EVTALKVPE	
EVTALKVPE	NOYFKMKP
DIO GENERAL GENERAL PROPERTY P	
TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCST	TCNOPEVG
GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFT	CSGKQESM
MSNVSVYQPPRQVILTLQPTLVAVGKSPTIBCRVPT	VEPLDSLT
LFLFRGNETLHYETFGKAAPAPQEATATFNSTADRE	DGHRNFSC
LAVLDLMSRGGNIFHKHSAPKMLBIYEPVSDSQMVI	
LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAANRRLP 5631 1053 290 SRVDDFVRPEPSRAEPSRSGRRPARRAATMSVFGK	
AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQE	LTANGGGK
TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQRE	ALENANTA
TEVLKNMGYAAKAMKAAHDNMDIDKVDBLNQDIADQ	ORLARRIS
TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLE	ISGPETVP
LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM	
5632 3 952 VVLGWSPPRRLWWGSLGAAORPAVPVSGLARSLHVS	TRRPHRRA
SVRVARGRLGVWAQPQPLLPRPVGSRRFMQPPGPPP	
FTFVSSADARDLSGSIASPDVKLNLGGDFIKESTAT	
GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVL	
NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWI	ITIWIFGS
LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPV	LLVVGSFE
VVSTLIKLFGVFWAAYSAASLLVGEBFKTKKPLLIY FLSLYTGV	PIFLLYIY
5633 771 460 OGCSKTMSVGRPFYRSSEFMEOLLGSHLHOVPFFCC	WILLIAM ON
CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYL	
LLILLSGHRPWGSSMV	WOLDIGOD
5634 1446 855 PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRL	SGRRAPAM
ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAED	SPDPSEVD
GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVV	LKVLTNFK
SSETEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSA	/LLQWHEK
ALAVGGLGSIIRVLTARKTV 5635 3 943 DPCDPSTATTYTCDERUSENDERLINGGUVYGNUGYGG	
DIGINOTINE TITLE THE PERSON OF	
RSLFHPFPVTRSGAPRAVLVGSSWPAKNVAPAVKVA	
GVRRAVLQLPGLTQVRWSRYSPEPKDPLIDKSYYRK: EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNM	AARETTER
LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNP	TTT PUONT
KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKI	MITTECED
KKHQRTLMPEKLSHKLLBAPHNQGPVIKRKHDLHKM	
HYRWW	
5636 2253 1143 LEDTICOHPPARKKLYLYHRKLREVERNGIPRLPKD	
LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGA	
ASLIRNKPGSADNIPNLKDSLEEGQVDDAGKALGVI	
YGSEBDCSSATSGSVGANSTTGGIAVGASSSKTNTLI	MQSSGFD
ALLHRIQEIRETQARLEESFETLKEHYCRDYSLIMC	LQEERYR
CERLBEQINDLTELHQNEIINLKQELASMEEKIAYOS QEALEACOTRISKMELQOQQQQVVQLEGLENATARNI	ZERARDI
LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVV	
HWDALFSYVERFFSSPR	* ***EDMK
5637 948 2532 MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPF	т.ррриг.н
HHHHPOHHLHPGSAAAVHPVOOHTSSAAAAAAAAAAA	
QQQPYFPSPAPGQAFGPAAAAPAQVQAAAAATVKAHE	
QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKO	PNVFQNL
VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYF	
LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHS	
IKPGNLLVMSNCVLKICDFGLARVEBLDESRHMTQEV	
PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQS	
ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVI	YTLSSQA

PCT/US00/34263

WO 01/53312

SEO	1 5 47 -6 - 4	I n 4/ - 6 - 4 3	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	w=irypcopnan, r=iyrosine, x=unknown, x=scop
	sequence	seductice	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		THEAVHLLCRMLVFDPYKRISAKDALAHFYLDEGRLRYHTCMCK
l			THEAVHIBERRITOFDFTERISARDALAHFTEDEGRERYHTCMCK
	1		CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF
5638	125	1155	ILEQQKGNRVPLCINPQSAAFKSFISSTVAQFSEMPPSPLVWE
2030	125	1122	DRKMSELDQLRQEARQLKNQIRDARKACADATLSQITNNIDPVG
			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
1			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIBT
			GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
			CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
1		i	MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
5639	125	1155	GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLK_WN
2039	125	1155	DRKMSELDQLRQEABQLKNQIRDARKACADATLSQITNNIDPVG
ľ			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
ŀ		1	TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
ł		l .	GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
			CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	
3640	200	.1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS
			IFRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
			NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTFDPRSPPNPDNIAP
			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPK
			LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
1	1		LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VPESEDL
5641	27	332	
2041	21	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA
			BIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAO
3002	199	1247	TIPCHNDFLYEFTHASVLMGLVEICVCSKTHSLKGLARGGAQ
			IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
	1		TWEVFGYCOELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT KANELLFLHVYEFDEVMFFKNVRCSTCDLRKPARSKHCSVCNWC
			VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
	1		LVHLVVMSDLYQRTYIDDLGHLHVMDTVFLIOYLFLTFPRIVFM
			LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL
			VAWPPSAEPOVHRNIHSHGLRSNLQEIFLPAFFCHERKKOE
5643	1	847	
3013		047	PSGGVRDVETRGPGSRAARGPRVVMHRRGVGAGAIAKKKLAEAK YKERGTVLAEDQLAGMSKQLDMFKTNLEEFASKHKOEIRKNPEF
			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLCLAEKNGYVTVS
			EIKASLKWETERARQVLEHLLKBGLAWLDLQAPGEAHYWLPALF
			TDLYSOEITABEAREALP
5644	83	1138	PRRMGSWVQLITSVGVOONHPGWTVAGOFOEKKRFTEEVIEYFO
3011	0.3	1130	KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
	1		
			YVAIEDKDMOOKROOFREWFLKEFPCIRWKIQESIERLRVIANE IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
			GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD
			ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
			RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL
5645	537	799	VQDSLDLHKGEKSESAELLROWAQELEENLNELTHIHQSLKAG
2042	337	199	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL
5646	3745	3328	YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
2049	3/45	3328	ABQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
			AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
			LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
5647	288	800	RAEGGAQ
3647	200	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH
			EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEQ	Predicted	Predicted end	I Amino said coment and down
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Clubania Anid D Changa Danapartic Acid, En
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Scrine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	1	\=possible nucleotide insertion)
1			CRVLPLPIFTPAKMGATKEEREDTPIQLQBLLALETALGGOCVD
	1		RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSOEAORG
5648	7	1518	VLSEL/CGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
1			APQSLPSSRMAPLGMLLGLLMAACPTFCLSHQNLKEFALTNPEK
1			SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAGS
1	ł		HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
			ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEBLKKDFDBLNVV
			IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
	1	ı	LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
	1		ECCALOKI LATI ACCORDINATIVA PRINCIPA PR
1		l	EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
		l	LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFABBEABLT
			QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
	i		LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
5549	1172	3006	DEGYFORLIGSVNSLLKELR
3043	11/2	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
	į.		KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
1			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
		İ	TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
			VPAKLGTQAEKDRRLKKKHQLTEDARRKGMPFAQWDGPTVVSWL
1			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMSTLETSTK
	1		TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
i			DARNLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
!			HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNNLLALG
			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQUIDAINEBIRMIQEEKESTELRABBIETRVTSGSMEALNL
1 1	1		KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
]			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSODSLHKGAKR
1 1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
1 1			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
1 1			ELWVGMPAWYVAACRANVKSGAIMSALSDTEICREIGISNALHR
1 1			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
! !	1		TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPOYRSYFMRCLU
			DARMLDHLTKKDLRVHLKMVDSFHRTSLOYGIMCLKRLNYDRKR
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
1			HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNNLLALG
1 1	1		TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*KARAKGPASESPRV*EGSGWEGPASP*TPGSTI.
1	1	J	AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1	1		WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
1 1			ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ
			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
			PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
1			PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
j 1			GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA
1 1			CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL
1			LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
1 1			CERCAR CERCENI VILIAR TURGETTE CONTROL CONTROL OF THE CONTROL OF T
		1	CEFCARSFRISSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW
5653	66	2401	HQRKHAETVAALRFPCBFCGKRFBEPDSVAAHRSKSHPALLLA
1		7401	RGRIQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
1 1			CFFQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
			GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHFDGSED
1 1	1	1	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ
			GWLLBLQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ

Doginning mocleotide location cortesponding cortespo	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nucleotide location corresponding to first la-Histotidine, la-Histotidine, La-Hi		beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding to first amino acid saino ac	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first tail amino acid amino acid residue of residue of residue of residue of amino acid acid acid acid acid acid acid acid				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid residue of amino acid sequence Sequence Sequence Codon, /=possible nucleotide deletion, v=Stop Codon, /=possible nucleotide deletion, v=Stop Codon, /=possible nucleotide deletion, v=Stop Codon, /=possible nucleotide deletion, v=Possible nucleotide deletion, v=possible nucleotide nu				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid amino acid sequence (codon, %-possible nucleotide deletion, %-possible) and locidide deletion, %-possible nucleotide deletion, %-possible nucleotide deletion, %-possible nucleotide lasertido; %-possible nucleotide lasertida; %-possible nucleotide lasertida; %-possible nucleotide lasertida; %-possible nucleotide lasertida; %-possible nucleotide lasertida; %-possible nucleo				P=Proline, Q=Glutamine, R=Arginine,
amino acid equence Codon, /-possible nucleotide deletion,possible nucleotide insertion) ES'ILSKTQSCYNERFEGRERHOUNSSITUTFAKSEYRGUER SYSDHSCUDE VORERFEYOCESSCSTSSSSSTETTENENTITHTES PYWAGCEGCTDERASHEGYTRYTHTOTKYYCKEYCTFFQGT EGGRAFTHITTHENENTYCKEYCTFFGGT EGGRAFTHITHTHENENTYCKEYCTFFGGT EGGRAFTHITHTHENENTYCKEYCTFFGGT THANNY 5654 3 598 THANNY THEFFGRERRGRERGANARKESTGGNYSHGERSVARHAN MMEPFYGGLASITARCOFFILDHKYRTQLQGOMBARYRSI FROMINANUCH GORDHANT GOR				S=Serine, T=Threonine, V=Valine,
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
BST-TERFORCHEFFERREND-DWS-SELT/PARKSEYMORPH STS-DISCOLD VOICER-PROCESSESSESSESSESSESSESSESSESSESSESSESSESS			sequence	
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5661 2 473 IMLYSPOGGYPKLROUPERAAALGASTIASADLPYTYRGSGL AGMAYTCDPKAFLSICTYTLVFLQLEPLASICQVFCTDSASROK ADPOVTSPHAPILAHAGGYVEKLGCQLPPNISASROKSHAYRCQP SLAVIMHERGMUNDUSGONYDRGT 5662 2 1318 LEKSBOKROSNOWANADASGLGGGGMILGVRCLLESVRFCSSA				
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ADPIVITGPHAPILAMAGGHVELLQCDLPPNISAEDKELRWYRCOP SLAVIHHIERGMUNDGEQNNQYBRGT S662 2 1318 LEKESGKCERGSNKGVWAAPABGLGGKKHLGVRCLLESVEFCSSA LEKESGKCERGSNKGVWAAPABGLGKKHLGVRCLLESVEFCSSA LEKESGKCERGSNKGVWAAPABGLGKKTHLGVRCLUST LEKESGKCERGSNKGVWAAPABGLGKKTH LEKESGKCERGSNKGVWAAPABGLGKKTH LEKESGKCERGSNKGVWAAPABGLGKTH LEKESGKCTH	5661	2	473	
SLAVHMHERGMDMDGEQKWQYEGRT 5662 2 1318 LRKBGRCRRGSNRGVWAAPABGLGGRGMLGVRCLLRSVRFCSSA				
5662 2 1318 LRKBGRCRRGSNRGVWAAPABGLGGRGMLGVRCLLRSVRFCSSA				
	5550			
	5662	2	1318	
PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF	1			PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
	residue of	amino acid	W=Tryptcphan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
			QNVBLKABKIKVIGNCDAKDFPIKYKERHPLBYLRQYPHFRCRT NVLGSILRIRSBATAAIHSFFKDSGFVHIHTPIITSNDSBGAGE
			LFQLEPSGKLKVPEENFFNVPAFLTVSGQLHLEVMSGAFTOVFT
		1	FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
1	ľ	I	ATTMMVLSKCPEDVELCHKFIAPGOKDRL*HMLKNNFLTISYTE
			AVEILKQASQNFTFTFEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGFQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCFGAERSLL
-			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
			NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP
			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
5664	118	572	KEHDNKLNQCLIPKKKK
2004	119	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG GPPPGNDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
		Ì	RAMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
		i	CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILHCERTSPAM:TSELPVLQDSTNETTAHSDAGSELE
			BTEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLEVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
			FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
ŀ			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
			VLDACSSEATHVVMEETSABEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACOR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
		İ	PSPVTTLSOLO
5668	691	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
			VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTQEGLSMHAHFQAYTPFIYLHARKRRGEIGD
			ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
ľ			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
5670	3	373	NSQ
3070	3	3/3	SSECLTMAWIPLLLPLLILCTVSVASYELAQFSSVSVSPGQTAK ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
			STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLOLLLDOKHEHLICWTSNDGE
1			FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	357	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
l	1		SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
1	1		FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP
1			NPPSHSRTSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
F 677			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIKSSAATTLAGPHTMEGESV
1			KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMRGESTSAVLSGPVLGALAFOHLNTDSDTEGFLLGEVKGR
30/2	1 1	204	AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
			LKKILSNVKKNVVGWYKFRRHSDOIMTFRERLLHKNLOEHFSNO
			DLVFLLLTPS:ITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
			MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN
			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
	1		QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
			MFLKVAVTTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLTHFRGVSECRRPPG
			KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKVT
1	1		LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYABSYGVIFVVDSSDEERMEETKEAM
	L		11F DIGGGIRINGIWANI 1ABSIGVIF V VUSSUBERMEETKEAM

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	
J	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, **Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ľ			SEMLRHPRISGKFILVLANKQDKEGALGEADVIECLSLEKLVNE
		i	HKCL
5676	2	930	FVSSPPPRPVQPARPGGF3LSCRRSLLCQVASTPAHVGVMRSPV
1			RDLARNDGEESTERTPLLPGAPRAEAAPVCCSARYNLAILAFFG
1	i		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
1			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM
1		i	LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
1			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
			WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
1	I	1	VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
1	1	I	GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
1			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIONSKRKGPEF
1	I	1	TREFESVLVDAFSHVARBADEGCKKPLERLLNIWQERSVYGGEF
1	1		TOOL VI. CHEDGYGDDDEN TREVYOU YDDDOOL OWERD THE
1			IQQLKLSMEDSKSPPPKATEEKKSLKRTFQQIQEEEDDDYPGSY- SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
1			DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	
3676	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
			GSGRTAAPRTRADPAAOSLMIMNKMKNFKRRFSLSVPRTETIEE
1			SLAEFTEGFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEE
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
5679	2		AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
	ļ	J	DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
			LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
1			FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
5680			MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLONRNSHTPLESLIHPQPSYKGPGIMFGKKKKKIE
			ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
			DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKBSQABGYNRSGINNHQAEDPRFCPSFCWMRSA
			ROTRPORLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
	l .		PTSAGLWIVYFIAVEDDK:LPLNSAERKPGVKHAPYISIAGDDP
	i i		PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
			LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
Į.			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
1			QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
1			PFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ
1			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
1			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITECLAWSVLISELAMATYTCITCRVAFEDADMORA
1			HYKTDWHRYNLRRKVASMAPVTAEGFOERVRAORAVAEEESKGS
1			ATYCTYCSKKPASFNAYBNHLKSRRHVELEKKAYQAVNRKVEMM
1			NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
1			EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
1			SEDERHOLC
5684	195	577	TWCFRGYLGPRVIMKALDEPPYLIVGTDVSAKYRGAFCEAKIKT
			AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
l			QBAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
1 1			LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPO
		1402	VKOEHPHTDSDLMHVKPOHEORKEOEPKRPHIKKPLNAFMLYMK
		ļ	
		J	EMRANUVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
5686	128	1181	RQLHMQLYPGWSARDNYVSPSSIPVALHS
2000	128	1187	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
1			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
			PHEABLMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, G=Glycine,
1.0.	location	corresponding	W-Wietidine T Jackson's W. T
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ł			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
1			RMDFLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST
1			STLTIHVLDVMDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
			NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
		Į.	YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAFPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
			QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS
		1	LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
			SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPQTSEPAPSP
			LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
1			PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS
1		1	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
1			VEDT
5638	1	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
1 -300	1	1 -20	*SUMTIDGLE *KUIDDGLGGIDE LDDLE L *****************************
1		1	*SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
1	1	1	DGYIPAVF
5689	1504	3	
3009	7204] 3	HBLSGKHISMVSGNTCNWHPGGHSPGGGGGGGTITSKDRGBIPAL
ĺ	I		IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPPQPCEGPRSTSRG
		1	GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH
			GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
ĺ			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
			PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
			GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
			EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
			GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
1			SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
			GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
			GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP
)		l	*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGGGROODPEP
1			DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
	l		GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SORT*ERARPRH
			PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPOLE
1			KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
			SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP*
1	·		GNPVR*LLLMP/GVA*RHGTSPFLGPSLGENGGOWDSGNLFGTP
			KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE
1 1			SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPPAG
1			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQNAKRGKKLVELPYTVKGMDVSFSG_LSFIED
			VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEON*S
i i			GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
			GVGVYVLLESVPLSYS
5692 -	1193	548	TQAWTRABKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIQK
	****	510	
			PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
			TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ
1			RLN_PVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLCS
5693	1200	2222	VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
2093	1258	1330	ALTVVPVRKGTTWKAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
			*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
i J	ļ		RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
			PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHR-GSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAGSAL
1			KVAGKPEGKATDKGKLAVKNTGLORSSSDAGRDRLSDAKKPPSG
1			LARPSTSGSFGYKKPPPATGTATVMOTGGSATLSKIOKSSGIPV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KPVNGRKTSLDVSNSABPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1	l .	l .	PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTFLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPRS
1			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAGSAL
	1		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
1	1	1	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
	l .		DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
	1		QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESCLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1 1			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAOSAL
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKLQKSSGIPV
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1 1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5697			DTTQCI
5697	1147	47	PSEALS PPACPS APAPERS I ISRLEGTS PATEAAPPPPE PVPAA
			QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
			SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
1 1			RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
			EGPIAAQMLSFVMDDPDFESEGSETQRRADDFPVRDDPSDVTDE
1 1			DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
			EGKTPSKENKKKKKKKKKEEEEKAAKKKSKHKKSKDKEEGKEERR
5698	2	566	RRQQRPPRSRERTAA
3030	4	999	GARAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
1 1			QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
1 1			GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
			NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
			FNO
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
0000		1440	EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
1 1			RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
1 1			DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1 1			TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
1 1			WTQKWTGE/SPAPGEEG\VAPAPROPTAEHGHCELTTESQYSNN
1 1			VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
1 1			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
1 1			GGSLGCR/SMLPASSGPPPAPGPRIAAGAHTSASARCPPAAAA
1 [GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGPGW*TLDPLPA
1			HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
			FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
1			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
1	i		E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDIOEFISPEINPOICSWLIFDEGAK/NHATGEDSIFN
1		720	KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
1	1		LBENTGENLHDTGLGNVFLDMTPKTOPTKOK
			TOWART TO MAKE A MAKE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
5702	3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
			ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
Ĭ	ĺ		SSDGPHPVITPSRASESSASSDGPHPVTTPSRASESSASSDGLH
			PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
			DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
	Į.		EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
	1		PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
	l .		PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ
		Į.	KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
1		l	GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
1			LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
1			PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
			RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVODKS**VSL
			DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
			ALPTGPRCW*APRGRTROPCGWPRLSSPHATADWGPGCPLSPSR
			GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDOC
ĺ			ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
			AGWPRHSPHDTOTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVECDORITAEEAISHEWI
1			SGNAASDKNIKDGVCAOIEKNFARAKWKKAVRVTTIMKRLRAPE
			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
1			SPOP
5705	23	562	GDYEFDSPYWDDISOAAKDLVTRLMEVEODORITAEEAISHEWI
			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			OSSTAAAOSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
1			KSDNVAPRRP*LPPOPOMEVPPOPLMAVSPOPPMEASLOPLMGE
i			SPOP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
			DYVANTONCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAOLLORTGAGACOEDYROYOAKVE
			WQVEKHKQELRENESNWAYKALLRVKHLMLHYEIFVFLLLCSI
1			LFFIIFLF
5707	28	609	GSPAPTPGPRRRPGRGTPSPGTRHHQGRAEP&PDAPERAPLRR*
1		333	MFAIQPGLARGGQFLGDPPPGLCQPBLQPDSNSNFMASAKDANE
1	i i		NWHGMPGRVEPILRRSSSESPSDNOAFOAPGSPEEGVRSPPEGA
		,	SIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG
			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGOPRPYLDLPA
1	**	1723	QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPOAKPKP
			PRCPFTAMPSPRTKOKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
1			RVSPASGGPRKEGROGSGG*AGGGGP\ARTHADLPCVGFVCSPP
1			LLK*SDSPVKOLPA\SGOGSGAGMPPVGSSDILRPRPTSVSGTG
1			RAAG*CSWQPAACCTPRSO*WAVARSPSRCSRW*ROSGR*RG*S
1			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
1			
	,		AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
]		AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
	i		
	j		QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAADPVSRCRPPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
1 1			PPRPPRDPARAS/SGGASGSPAASCSCSCRAPARPASS/GEAPA PPPRPEPPPPARRP
5709		2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
1 2,02	4	203_	LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS
]	0.0		LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
			DELINE V CHANT V V V DRAGEWALGGLDIN 1 SANGGROGG P P R RG 1 P E

SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
i			ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM
1			SNRFVRTNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
		1	VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
			MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
			NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLOAKDEOGPI
			RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDFFAPSRVAGV
			LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS.
1			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
i		ł	VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1			TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1			DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
1			GAKLPGATS*RYTAGGRV
5710	1	562	
3710	1 1	362	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
1			VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
			\LKGHDYMRNIVHLPVFLMSRGL/RQ/LQENFS*LQQQMETFHA
			QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
			CIAIQFNINKDDAT
5711	1526	1130	RRHPFQWTTVTQBAFSHHDVAFTSTPVLFYFDSAQPFIVKSESS
1			SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQ3IF*LLM
1			LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
		l .	QIL
5712	3	1391	GRKLFQSLDISER_KFLLTLDCVDDTLIVLAFEHGCLDIIKELP
1			ETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
į			SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
1	ı	1	AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGOGRDRSS/
1			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNOIWK
1			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
1			EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWOGLD
	1		SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIOEY
		l	LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQBGQQL*AKLPRDFRR*FQILGPMEGH
			TACRCSRRGACVOHLPREDIRAAE*DPHLREVWPGLPTSSATSP
1		l	*RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSODAGGSSSSSTNGSGGSGSSSGPKAGAAD
1 2,22		""	KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
1			HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA
1	ı		
5715	131	1979	MA
5,13	131	19/9	ESASQQKRSKCLILTLKLELSGSAPKKTSARP3SSLWLPPHSQE
1			QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
1			GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
1			DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
1	1		PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
1	l		QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
1	l		TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
1			YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG
1	l		L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
1	I		PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
1	l		VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAOALE
1			EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT
1			GLT/GVPGTDPKRGGRKPGOSGOETOGPTVWSGPESPLOPKP*E
1 :	1		RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
			TDLTEAOTSOH
5716	1711	1370	RVFSLLCEGPGHCYOGAVCREACAAASPGLDSAAEPHRLCEHTD
1			*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
-			RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD
		1403	EGPGALVLESDILLGQDLEFEREEEEEEGDGNSDQLMGFERDSE
			no-communications and selection of the s

SEO	Predicted	Predicted end	I Series and A Committee of the Committe
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
1	i		RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
1			CTIVOOUT KTUMOSUUGGPCCGAGGPGGGPLLEPPRLLYSCRLCTFV
			SHYSSHLKRHMOTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
	!		RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
	1		Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
	1		AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
1		1	RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGBKPYKCPL
]	1	1	CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
1			S**STADPLHL
5719	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
1 - / 2 /		1 .20	I COCUMEN WELL DEFENDED AND COUNTY OF COLUMN AND COLUMN
I	1	1	LSQGYNVKAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5720	1		IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5/20	1 1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
1	I	1	\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
			GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
į.			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
1			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQG1LLKRSGKSLNK
1	1		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
			KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
			LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
			CHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
		***	WHOSE COLLEGE BRANCH TO STREET
	l .		VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
5722	88	1043	SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5/22	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPCGAAQSPHRGRRHGGGGAGLPPPRSPRFP
	,		QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1 1	l I		GRARGOAGLLGROGOGGRGAERERAALQARRGRRPGPEPDQSCG
	l l		GRPRRAAAAPGRAPADPQPPAPRFAPADDVRFPADAPAPAPAPA
			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
1			KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
	i i		QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPEOSCG
			GRPRRAAAAPGRAPADPQPPAPRPAPAPADVRPPADAPAPAPA
			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
1 /			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	
5,74	, ,	1041	FINEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
1 1	l J		KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAEEAADLDGEID
1			LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
1 1	1		MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKCEAELGEP
1 1			DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP
1			ADTH\DPWRPEARHGELERERARREERRKRFGMLDATDGPGTE
1	,		DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK
1			QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSCKEASDLLEC
1			NRLLQDQLRVALGREQSAREGYVLOATCERGFAAMEETHOKKIE
1 1			DLQRQHQRELEKLREEKDRLLAEETAATISAIBAMKNAHREEME
1 1			RELEKSQRSQISSVNSDVEALRROYLEELOSVORELEVLSBOYS
1			QKCLENAHLAQALEAERQALRQCQRENQELNAHNCELNNRLAAE
1 1			ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTOLC
1 1			TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE TOPPOGGA AND CHARGE
5725	2	2010	TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
2143	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSCPVG
1 1			SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
1 1			KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
L			PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	[A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S-Serine, T-Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,
-	sequence		\=possible nucleotide insertion)
			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSMIN NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPFMMPG
1			SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
			TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
1	-		TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
1		1	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
1	j .	}	GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDOASCEVLTVKKK
			AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVOPRGSG/LPG
			NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
			GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
1			GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
1			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
			EPPQVPEAGEEDAVPAEEGPGGTPETQADQVRERPEAHLAEGGA
			KGSPRRLADPODLPAGOMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
i l			CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
			QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV
			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
			CDYLQGFQILCDLHDGFSGVGAKAARLLQDEYSGRGIITWGLLP GPYHRGBAQRNLYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
1			MVHL\ADMLSFCGKKVVTAGALIPFPLAFGQSLPDSLMQFGGAT
1 1			PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSOLTPGTPPPSA
1 1			LHACTTGEEILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
1 1			SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
			KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ
			GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
			EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
			KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
1			PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
1 /			LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
			QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK
5733	1	460	ALLDAA
3/33		460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
			AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS
1			FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLEVLETTANNEFVLIPAYSKNRAYAIFFIVFTVI
1	,	500	GSLFLMNLLTAITYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
1			SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
1 1	'		GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
1			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
			VFIVYYLLEMLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
			TL\VCTDCHTQAGGRRWW/RLLSLWENTRMLNML;VFRFLRIIP
			SMKPMAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL
			ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ
1 1			YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
			RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
			LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

SSO Predicted Predicted end Amino acid segment containing ID beginning nucleotide Ralanine, Cacysteine, Paspa No: nucleotide location durante Acid, Farbenylalanine corresponding Helistidine, I isoleucine, K-L	
NO: nuclectide location Glutamic Acid, F=Phenylalanine	signal peptide
	rtic Acid, E=
	, G=Glycine,
	ysine,
corresponding to first L=Leucine, M=Methionine, N=Aspi to first amino acid P=Proline, O=Glutamine, P=Argi	aragine,
	nine,
	b,
	cnown, *=Stop
amino acid sequence Codon, /=possible nucleotide de sequence x=possible nucleotide insertion	elecion,
TARLSVTPPNLLPTVSFPQPDLPDNPVYST	1)
QES**ILPDSGIFIP*T*TSYLQSTTHLRRI	ITEKLASDLRANKN
5737 290 1041 KACLHLLSSFLTSNFLFNPLLPDSLYSVEAR	ANDPUDERK
LQTLMRLAAGFQYSSHKDPSLSAKEKHTDYI	CSQRANLGPCRRKR
RTADGSCGRGPDGAHHPGPKSSSWRASRLLi	INEARGPWPGWVG×
RDLECGTPAPLOLEIPPOPRGHPAPIPTGO	CODDOCOCOCOCO
ETRPLTDGRR*PGVRPVGWTPAHPAGTLRP	GT KEDGE GYGT CAN
APSPTSQGCCEGRCDAVPKHRAWRTPLCSO	TOTAL D TOMOGRA
5738 8 460 DTLSLNCTLP3TLPMTPSF*LSFL*FPGLAN	DECEMPANDO NOT
VTLWYRPPDILLGSTDYSTQIDMW*GQVEVY	CORDORAGE TANDA
ATQPAAFLFTVPSLPRGVGCIFYEMATGRPI	FPGSTVEROLHET
FRILSEEAWALCAVETHR	
5739 1 1222 SFORRGIRWNVHTLHPHPRAVWAGIGRGHGS	*ALLGRAPAPAT.C
FPTLLEFLESLEPDLPALRAMGLHLWAAGPG	THPAGISDLLARV
SAEVDGPVPGYLSSPOSITDTCLYIFTSGT	GLPKAARISHLKT
LQCQGFYQLCGVHQEDVIYLALPLYHMSGSI	LGIVGCMGIGATV
VLKSKFSAGQFWEDCQQHRVTVFQYIGELCF	YLVNOPPSKAERG
HKVRLAVGSGLRPDTWERFVRRFGPLQVLET	YGLTEGNVATINY
TGQRGAVGRASWLYKHIFPFSLIRYDVTTGE	PIRDPQGHCMATS
PGEPGLLVAPVSQQSPFLGYAGGPELAQGKI	LKOVFR PGDVFFN
TRDLLVCDDQGFLRFHDRTGDPFRWKGENVA	TTEVAEVFEALDF
5740 265 231 PAYWLKVPTLCLESKTDLREKASHVSAOLOG	
	evrglagalwm*A
YVYERVYN*NISRMVHALEQKRHPAGLSSSM	ALQLNPCLGMLMA
LQSELHKLYDEETQSWVSGSACGGYP 5741 1 650 PRKTMRRGVLMTLLOGSAMTLPLWTGKPGDP	
	PPPLOGAIPASGD
YVARPGDKVAARVKAVDGDEQWILAEVVSYS EGKERHTLSRRRVIPLPQWKANPETDPEALF	HATNKYEVDDIDE
TCFYRALIHAPPQRPQDDYSVLFEDTSYADG	OVEOTATIVE LAGI.
ACKEPKKK*CRLADSPSPNDTGQDSRGRAGI	TOLDDIANA CKIAA
5742 2 362 TQSVKEILKRNPNVNLTDKDGNTALMIASKE	CUTTURE I DEC
TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQ	WALLIAGORDAN
TALYWAVEKGNA THURDILOCKIPDTET CTKD	G
5743 2 415 GKTPEGIDAIBBIBIDLEETERBISPQENGL	EFUNDIGENOTOL.
KATGREISPREKTPEVIDATEEIDKDLEETG	RREISPERNGPEE
. VKPVDEMETDLKTTGREGSSREKTREVIDAA	EVIETDLEETERE
ISPQE	
5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPD	LTTGTPLOMTTIA
VFTTANTCLSLTPSTLPEEATGLLTPEPSKE	GPILTAESETVLP
SDSWSSAESTSADTVLLTSKESKVWDLPSTS:	
POPGASDTAVPEQNKTIKTGQNDGIPMSMKN	EMPISQLLMIIAP
SLGFVLFALFVAFLLRGKLMETYCSQKHTRI;	DYIGDSKNVLNDV
QHGREDEDGLFTL	
5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQK	
KGDYLETCGYKGEVNSRPTYRMFDQRLPSET	
VENRLPQWLPAHDSRLRLDSLSYCQFTRDCF.	
YICGSHGVEHRVYKHFSSDNSTSTHQASHKQ	IHQKRKRHPEEGR
EKSEEERSKHKRKKSC3EIDLDKHKSIQRKK	TEVELETVHVSTE
KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQ.	RKIEEENLWDQSI
5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAI RAGERRFPCPVCGKRFRFNSILALHLRTHOPI	
LEERALLREARLGRARSSGCMOATPATEGLAS	
YCKGKPRTSAERERHLHILHRPWKCGLCSFG:	ALTERDACACHER
YCKGKPRTSABRERHLHILHRPWKCGLCSFG: AHGAPERPLAATSAAPPPQPQPPPQPEPR:	
YCKSKPRTSAREERHLHLLHEPWKCGLCSFG; AHGAPERPLAATSAAPPPQPQPPPPQPERF EATPTEAPAADEEPAAPPERFCQVCGCSFTG;	SWFLKGHMRKHKA
YCKSKPRTSARRERHINILERPRIKCALCSRG AHGAPERPLAATSARAPPOOROOPEPPE EATPTFAPAAPBEPPAPPEPRCOVCOGSFTO: SEPHACOV	
YCKSPRTSARRERHALIHBPPKKGLCSSR ANGAPERIAATSAPPOPOPOPOPPEPER EATVIDAPAAPERPAPERFOVOGSFTO: SPERACVY 2 1326 PRHYSTLCHFELIPSTGSTAKTOGRNWLFTG	NCLYGNTCRFVHG
YCKSYFFTSARRERHINILERPRICALCSRG AHGANERPIAATSARAPOROGOOPPOCTER EATPTFAPAAPGEPPAPCOVCGGSFTO: SEPHACOV	CLYGNTCRFVHG

SBO	Predicted	Predicted end	Amino acid segment containing signal pertide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
[to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	amino acid	sequence	Codon, /-possible nucleotide deletion.
ł	sequence	"	\=possible nucleotide insertion
		_	SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREETTIK
1			KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
1			AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
1			KYKVKDRIEEKTRDGKDRGRDFERQR3KRDKPRSTSPAGOHHSP
1		l	ISSRHHSSSSQSGSSIQRHSPSPRRKRTFSPSYQRTLTPPLRRS
1			ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
1			ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
1			RE
5748	934	473	SEGPOVPYKGLAPTLIAIFPYAGLOFSCYSSLKHLYKWAIPAEG
1			KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGCFEHARAA
1			FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
1			FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
	1		SASSTYSSABERMOSEQIRKLERBLESSQEKVATLTSOLSANAN
į.			LVAAFEQSLVNNTSRIRHLAETAEEKDTELLDLRETIDFLKKKN
			SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
			GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIOF
			HLEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
			QENYVAQLILDVRREGDVLSNCEFTPAPTPOBHLTKNLELNDDT
}			ILNDIKLADCROFOMPDLCAEBIAIILGICTNFOKNNPVHTLTE
1			VELLAFTSCLLSQ=KFWATQTSALILRTKLEKGSTRRVERAMRQ
ì			TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIPEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATPPAPALPGLMYRALYAFRSAFPNALA
1			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
!			DVLQAIDRAIBAVHNTAMRDGGKYSLEORGVLOKLIHHRKETLS
i			RRGPSASSVAVMTSSTSDHHLDAAAAROPNGVCRAGFEROHSLP
ł			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDRRA
1			LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVANAGPWRGPVHSVGGGGRAALHGARLPCLSGAAT
1			VEREMELRHKNEMLRVETBARARAKAERENADIIREOIRLKASE
			HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
	١ ،		AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GOEAFEKLNYLDIGEIKKRPMEVVNTRVKPVIHSRINVSARFRK
1			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
			TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEPAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
			ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
			WPTPATPSPLTAPPSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PEVELPLKKDGFTSESTTLEALLEGEGVEKKVDAREEESIQEIQ
			RVLENDENVERGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
1			DOETRS PPNHRNENHR POKGPDGTVI PNNYCDFCLGGSNMNKKS
			GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLOALFAHPLYNVPEEPPLLGARDSLLASORALRYYRRKVAR
			WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
1			HLKLVLRFSDFGKAMFKPMRQQRD3ETPVDFFYFIDFQRHNA31
			AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHROVVFENGTLKLTDVQKGMDEGEYLCSVLIQPO
	l l		LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
			ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFFGHESRATEALC
L			WARGORLFSAGLNGRIMEYDLQALNIKYANDAFGGPIWSMAASP

-	SEO	Predicted	Predicted end	I being agid assessed
- 1	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- 1	NO:	nuclsotide	location	Cluberia Baid T Phone 2
- 1		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
		amino acid		P=Proline, Q=Glutamine, R=Arginine,
		residue of	residue of	S=Serine, T=Threonine, V=Valine,
ı			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
L		sequence		\=possible nucleotide insertion)
				SGSQLLVGCEDGSVKLFQITPDKIPV
П	5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
- [ı		MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTF
H				NKDVGADLVCYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA
		l	l	DKLIAEGTVTLQEFEEBIAKYDRICEEAYGRSKDKKILHIKHWL
- 1		i .		DSPWPGPFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
- 1				KIHTGLSRILEGRADWTKNRTVDWALAEYMAFGSLLKEGIHVRL
		l		MODIFIED CONTOURNESS AND ANY ADMANDAGE THANGS LLKEGIHVRL
				NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
1		1		SSLSEYGVLGFELGYANASPNALVLWEAQFGDFHNTAQCIIDQF
- 1				ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD
H	5760			SDAYPAFTKDFEVSQL
П	5/60	1	1221	VRDITSDSLSLSWIVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
- 1				GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAFGKDEEMA
-				PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVFEGQFDHF
				LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
				QRVGPVSAIGVTAAEBETPTPTEPSMEAPEPPEEPLLGELTVTG
-1				SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
	- 1			VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPOEDVDETPSP
-				TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
1				VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR
	ĺ			RLGPVSAIGVT
۰	5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRECODON
	Į.			VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKSGFGSML
	- 1			RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKOOAERE
	- 1	1		ARTHOUNTERN TON CONTROL TON CON
	Į.			AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
ı	- 1			GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
				EGLETARGSNSESSDDDSERAPSTSGMGFHAFKIGSNGVEMAAK
1	- 1			FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
П	- 1			EHMESRMVTETEETQEKKAESKEPIEEEPTGAGLNKDKETEERT
				DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
\vdash	5762			AELELLGLEKLKCELMALGLKCGGTLQ
	5762	2	344	GSTGQTPLHSQGGGGGGGGGRRTPRGMPXEKYEPPDPRRMYTI
1	- 1			MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
L				SLSRIPSDIAKLHNLVYLDLSSNKIR
П	5763	3	429	LDKDTGLIMLIARLDYRLIORFTLTIIARDGGGERTTGRVRINV
1				LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
П	- 1			ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
П		i		TVMAMDAGN
г	5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVERIVSVRGPSLEEK
1	1	- 1		LRSQLYQGDFVHAMBGKDFNYEYVQREALRVPLIFREKDGLGIK
1	- 1	1		MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGT3MSMSQFVRYYE
				TPEAORDKL
\vdash	5765	3	825	QKILRLNNSHOPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
1		-	525	WALDALINGONGE FLOODNOAD COGPASSGAGATAALADGLKFAS
П	- 1			VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
1	ļ			STGKRQEVQGRPGRATGMNSALGQSVSSGGSGNPNSNSTSTSTS
Í	İ			AATAGAGSCGKSKHEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
1		j		GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
1	- 1			GEVSKSAPDSGLMGNSMLVKKBEEEEESHRRIKKLKTEKVDPLF
\vdash	5766	1608		TVPAPPPHV
1	5/66	1608	663	SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL
1				AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
1		1		PTELPHPSEGNDEKAKEAGEGRGDSTGEAGAGGGVEPSLEHLLD
1			1	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
1	- 1		1	TEELAVARPEDTVGALKSKYFPGQESQMKLIYOGRLLODPARTL
1		1	ļ	RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
1	1			SLMVPVFVVLLGVVWYFRINYROFFTAPATVSLVGVTVFFSFI.V
1		1		FGMYGR
Г	5767	2	892	NFRATPRPPTRPELRTGTRVILWYLDWRALMKRKRMKANIKLVG
1				SGFPLPSSDLDDSLTEBIDEKIGFRNDANFDWQNVADFRDAGGS
1	- 1	1	1	LTEVKVEEEERDPQSPEFEIEEEEEMLSSVIPDSRRENELPDFP
-				WOLDLETBEBERTHOOAT LOSKKENETLDEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K-Lysine,
1	to first	amino acid	L=Leucine, M-Methionine, N-Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	
	acdmence	-	\=possible nucleotide insertion)
	ľ		HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
			LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
	1		NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
5768	3	476	FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5/68	,	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
			AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
		1	SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
5769	3.9		WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
1	ŀ		TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
			DRCVEVIAKEGONLKELYLVSCKITDYALIAIGRYSMTIETVDV
		l	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
			PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
1 1			FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
1			AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
			WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGFSSRACSNGSQDTFKACYSGTSTPS
			FEGSHCSGSDHSSLGLEQLQDYMVTLRSKLGFLEIQQFAMLLRE
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
1 1		Į.	LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
			AFHRLLADITHDIE
5772	148	383	EFNLALVSFSHPQIKAEDDQPLFGVLLSLSGGLFRSNLLTQDNG
			ILTFSNLVTCSAIYHLPVFPBREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEM1TGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
			LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
1 1			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
			RRLNISYTRNMTLKDGKNSK
5774	. 2	592	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
			VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
			KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
			RDGYGTLSLFDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
			EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
			RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRIVELRLGGNF
			IIHISRQDFANMTGLVDLTLSRNTISHIQ?FSFLDLESLRSLHL
			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
			EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GQDPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
			YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
-			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
	ļ		YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
			NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
			GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
			WAPLGAPERPEHLINRVLERLAGGATRDSAASDILLDDIVLTHS
	l l		
			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKOACTAMTJJHFT.DT
			LFLPTEKFLQELHQYFVRAGGMEGPBGLGRKQACLAMLLHFLDT YQGLLQBEBGAGHIIKDLYLLIMKDESLYOGLREDTLRLHOLVE
			YQGLLQBEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
	,		
			YQGLLQBEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPBENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Tsoleucine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
			PLPBEIQVSPGDTEIHRVSPEDVANHLTAFHWELFRCVH3LEFV
5779	453		DYVFHGE
5//9	138	1671	EAVQVLIKHSADVNARDKNNQTPLHVAAANKAVKCAEVIIPLLS
			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
	1		ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
			NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
!			NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1		i	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
1	1	ł	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
			QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
ł		ľ	KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
	j .		ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
1			EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
5780			RINSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
1			EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
1			DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHCQACLREK
5781	19		KKGLNVIGASDQSPLQSPSNLRDNP
2/07	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
1	l I		PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
1			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRFLDRSPPLGQ
1			VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT
			QHSIHTVTCKSPRQKEDRSPKPPQAPKHPEBHGRQS\QAPPPLP
	1		VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
E793	5176		NIMD
5782	5176	1237	NIMD DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
5782	5176	1237	NIMD DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
5782	5176	1237	NIMD DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPV3QSEISEPSAVPTDYSVSASDPSVLVSERAVTVPEPP
5782	5176	1237	NIMD DESMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEGSALTAENTMPTEVPSLPSEESV SQPEPPVSGSEISEPSAVPTDYSVSASDESVLVSBAVTVPEFP PEPSSITTTPVSSAVVASEETEVVPERPVTCAVSETPAMSAEPT
5782	5176	1237	HIMD GRAMMSHAADSYTDSYTDTYTSAYMVPPLPPERPJYMPPLPPEE PPMTPPLPPEEPPENPALPTEGSALTAENTATPTEVPELPSESS GOPEPPVSGSETSEFSAVPTDYSVSSADSEVUSSRAVTVEFF PEPESSIT_TPVESAVVAEEHEVVPERPVICMYSTFAMSAEPT VLASSEPVMSETATFTSSKASGNVASEVSTSLVPAVTYPVLA
5782	5176	1237	INIM BRIMASHARBYTDSYLDTYTEAYMYPPLPPEEPPMPPLDPEE PPKTPPLPPEEPEMBLAPTEQSALTAENTWTEVPSLPSERSV SQPEPPVSQSEISEPSAWPTDYSVSASDSWLVSERAWTYDEPP PERSSIT_ITVESSAVVABENEVEREPYTCHSETPMASEPT VLASSPPVMSTAETTDSWEAGHVASEVSTELLVSAVTTPVLA SELIEPPAMASPTAWTESWEAGHVASEVSTELLVSAVTTPVLA SELIEPPAMASPESAMAVLESSAVTVLESSTYVTL
5782	5176	1237	NIMO DESMMSHABUSYTESTUTTTEANWPPLPPEEPPIMPPLPPEE PMCPPLPPEEPPEGDALPTEGSALTAENTMPTEVBLESERSV SORPEPVAGSETSERSAVPTUSSASSASSISSUSUSSAATVUSEP PEPESSITT.PPVESAVVABEHEVVERPPTUMSETFAMSABET LASEPPMAERATETBORKSAGTASSEVSILLIPAVTTULA ESILEPPAMAARESMALUSSANTULESSITTULESSITTUL ESILEPPAMAARESMALUSSANTULESSITTULESSITTUL ESILEPPAMAARESMALUSSANTULESSITTULESSITTUL
5782	5176	1237	NIMO DESAMONAADSYTESTILTYTEA/WYPLPPEPPYMPPLPPEP PPHPPLPPEPPED AD HIPOSALTAENTMYPEVPELDESENSY OCREPPYGGET IS REPAYPTISYSAS DESKUTSSANTYVEEP PEPESSTILTYVESAVYABENEVVEREPYTOWS ETPHANGAEPT BEFESSTILTYVESAVYABENEVVEREPYTOWS ETPHANGAEPT BEFESSTILTYVESAVYABENEVVEREPYTOWS ETPHANGAEPT BEFESSTILTYVESAVYABENEVYTESTILTYTESTILTYTAE ESSUTYTEEPYVAEPTVITEYPYTESTIVTYTESTILTYTE BESTUTYTEEPYVAEPTVITEYPYTESTIVTYTEFTAISTEM BENTYEEPSVENOSESTUTYSERSTIVTSETTYTETT
5782	5176	1237	NIMO DESAMSHABUSYTESTIDITERAYWYPLPPERPIMPPLPPEP PMTPPLPPERPERDERAPTEGALITAENTMYPTEVPELDESERSY SORPEPVAGSETSERSAYPTISSYSAEDSEVUSSERSAYTVEEP PSPESSITT.TPVESAVVAEHEWVPERPVTCAVSTFRMSAEDT LASEPPMAGERSTTSIDAESGATASEVSTSLLUPAVITVILA ESILESPPMAGAPESSANALESSAVTULESSITVTLESSITVTLE ESILESPPMAGAPESSANALESSAVTULESSITVTLESSITVTLE PSWITVEPPMAGEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGENTAEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGENTEEDVILESPWISALESSYVLEPAVISLE PSWITVEPPMAGENTEEDVILESPWISA
5782	5176	1237	NIMO DESAMONHADSYTESTIPITEANWPPLPPEPPIMPPLPPEP PPMPPLPPEPPROBAPTOGRATAENTMYPTEVPELDESSSY SOMEPPVÄGES INFRANTVEREP PERSSITLÄPVERAVVAEBHEVVEREPTIMOSTEPHNSAEPT ALASEP PMSATATTIOMHAGENTVAESTITLAVSTYTTYLA DESAMONTATIONAS ON THE STATEMAN DESAMONTATION DESAMONT
5782	5176	1237	NIMO DESSMONHADSYTESTILITYTEAVMYPLPEPEPIMPPLEPEE PMTPELPEEPENEGALPEDGALTAENTHYTEYPELESESSY PMTPELPEEPENEGALPEDGALTAENTHYTEYPELESESSY VERSTENEGALPEDGALPEDGALTAENTHYTEYPELESESSY VERSTENEGALPEGALPEGALWA ERESTAENTEEPENEGALPEGALPEGALPEGALPEGALPEGALPEGALPEGALP
5782	5176	1237	NIMO DESAMANADAYTESTIPITEANWPPLPPEPPIMPPLPPE PPMPPLPPEPPROBAPTOGALTAENTMPTEVESLESSRY ORDEPVAGES ERFEAVPTOSASATAENTMPTEVESLESSRY DESAMANADAYTVESP PERESSITATPVSSAVVALESERVEDERVICTOWS FTEMASAERT LATURASEPPMAGEATETIOMASAGATASTISTILLAWATUTTULA ESILUEPPAMAAPESNAVLUSSRYTULSSSTYTTLESSTYTTL ESINUTY EEPYMAGEDVIT PWAALESSRYTULSSTYTTL LESS INGSINWEITH ORDERVICTORY ORDERVICTORY ORDERVICTORY LESS INGSINWEITH ORDERVICTORY ORDERVICTORY ELHCOPTESERVEN DITTORY ORDERVICTORY ORDERVICTORY ELHCOPTESERVEN DITTORY ORDERVICTORY ORDERVICTORY TORRESPONDE TO THE TORRESPONDE TORRESPONDE LOSEKLIPSETKOSTULTYPOVESDAGATETS STOPPALERO AND TRANSPORTATION ORDERVICTORY TORRESPONDE TORRESPONDE TORRESPONDE LOSEKLIPSETKOSTULTYPOVESDAGATETS STOPPALERO AND TRANSPORTATION ORDERVICTORY TORRESPONDE TORRESPONDE TORRESPONDE LOSEKLIPSETKOSTULTYPOVESDAGATETS STOPPALERO AND TRANSPORTATION ORDERVICTORY TORRESPONDE TORRESPONDE TORRESPONDE TORRESPONDE LOSEKLIPSETKOSTULTORY ORDERVICTORY TORRESPONDE TORRES
5782	5176	1237	NIMO DESMONHADISTUTITTA YMVPPLPPEP PYMPPLPPEP PYMPPLPPEP DEG ALPTOGALTAENTH/PEVPELDESESS OFFEPVAGES EERSEN PYTISTASABDESUURSALTVEEP PAGES EERSEN PYTISTASABDESUURSALTVEEP YLASEPVAGES ERSEN PYTISTASABDESUURSALTVEE ESSANTATION OF THE STATISTAS OF THE STATISTAS ESILEEPPAMASPESSANTALESSATVULSSITYVULSSITYVUL ESSANTYFEPPVAGED YVITIFYESTATYTO STATISTASTON ILESSITYSTASTON OF THE STATISTASTON
5782	5176	1237	NIMO DESAMANADAYTESTIPTTEANWPPLPPEPEPIMPPLPPEP PIMPPLPPEPPEROPROPALPTEGALTAENTMPTEVESLOSERSY ORDEPWAGES ERFEAVPTIESSANDESVUNSSANTVEEP PERESTITATIVESAWALEENEWVEERPVICTOWS FTEMASAEPT LATERIANTSANTOMASAGATOTISLASTATIVESTIPTAMASAEPT SAUGHEPMAGESTATIOMASAGATOTISLASTATIVESTIPTAMASAEPT ESVUTYEEPYMAEPYNTEMASEVSTILASTATIVESTIPTAMASAEPT LESSITATIVESTIPTAMASEVSTILASTATIVESTIPTAMASAEPT LESSITATIVESTIPTAMASEVSTIPTAMA
5782	5176	1237	NIMO DESAMONHADSYTESTETTTANWPPLPPEPPIMPPLPPEP PMTPLPPEPPEM ALPTEGALTAENTMYTTEVPELSERSY OPPPPVGGETERFAN PTIGSVASDBORGUTSENTATUTEEP PMTPLPPEPPEM ALPTEGALTAENTMYTTEVPELSERSY ULASEPPWGETAETTGBEN ALPTEGALTAENTMESTPTAGAEPT ULASEPPWGETAETTGBEN ALGERIAGETESTETTE ESSELVEPPMAGESMANULESSTATUTSESTUTYLESSTYTYL ESSELVETYPEPPVAEPTSYTESTEN ALGERTYSESTYPULESSTYTYL ESSELVETYPEPPVAEPTSYTESTEN ALGERTYSESTYPULESSTYTYL ESSELVETYSETYSESTANICHESSTATUTSESTYTYL ESSELVETYSETYSESTATUTSESTYTYL ESSELVETYSETYSESTATUTSESTYTYL ESSELVETYSETYSESTATUTSESTYTYL ESSELVETYSETYSESTATUTSESTYTYL ESSELVETYSETYSESTATUTSESTYL ESSELVETYSETYSESTATUTSESTYL ESSELVETYSETYSETYSETYSESTATUTSESTYTYL ESSELVETYSETYSETYSETYSETYSETYSETYSETYSETYSETYS
5782	5176	1237	NIMO DESAMANADAYTESTETTTÄÄNYPPLPPEPETYPPEPETE PPETPETPETPETPETSAMATALATITYPTEVESLESERSY ORGENPVÄGESTE ERPRAYPTEVESVASIDESVUNSAATVEEP PETESSITLÄPVESAAVALEEREVVERPYTÄMSETPTTAMASETT LASEPPÄÄRETTEOMASAGATASETSILAPVATYTYLÄ ESILEPPÄÄRETTOMASAGATVILESSITYVILESSITYVIL ESILEPPÄÄRETTOMASAGATVILESSITYVILESSITYVIL ESILEPPÄÄRETTOMASAGATVILESSITYVILESSITYVIL ESILEPPÄÄRETTÄNETSILANKATASETSILAPVATYTYÄRETYTTÄ ESILEPPÄÄRETTÄNETSILANKATASETSILAPVATISSITYVI ESIVYTYEEPÄÄRETTÄNETSILANKATASETSILAPVATISSITY LASEPÄÄRETÄNETÄNETÄNETÄNETÄNETÄNETÄNETÄNETÄNETÄN
5782	5176	1237	NIMO DESAMONHADSYTESTILITITANWPPLPPEPPIMPPLPPE PPMPPLPPEPPEM AD ADPTEGALTAENTMYTEVPELDESENSY OCREPPVOGES IS REPAYPTICS VAS BODSYLVESS ANTWEEP PEPSSETTLTPVERAVVAIRENVEREPVOTAMESTPHAGARPT PEPSSETTLTPVERAVVAIRENVEREPVOTAMESTPHAGARPT EPSSETTLTPVERAVVAIRENVEREPVOTAMESTPHAGARPT EPSSETTLTPVERAVVAIRENVEREPVOTAMESTPHAGARPT EPSSETTLTPVERAVVAIRENVERAVENSTTUTESTPHAGARPT EPSSETTLTPVERAVVAIRENVERAVENSTTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMKOINLISSEDQHILAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMINISTERIAMESTRIAFRENVESTOTUTESTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMESTAMINISTPHAGARPT ILESSITAMEST
5782	5176	1237	NIMO DESSMONHADSYTISYTUTYTEAYMYPLPPEPEPIMPPLEPEE PMTPELPPEEPENEDALPESCALTAENTHYTEYPELESESSY PMTPELPPEEPENEDALPESCALTAENTHYTEYPELESESSY PMTPELPEEPENETALPESCALTAENTHYTEYPELESESSY VERSIGNING PARTICULAR STATEMENT OF THE STATEMENT O
5782	5176	1237	NIMO DERMONHADISTICITITATIAN PPLPIPEP PINOPPLPEP PINOPPLPEEP PERO ALPTEGALTAENTHYPTEVELLESERSY SORPEPVAGES ES FARA PTOTOS VASA DESVUMSEANTIVE EP PEPERS ITLTIVERAVVALERIEVVEREP VICTOMS ETPHAGA EPI PEPERS ITLTIVERAVVALERIEVVEREP VICTOMS ETPHAGA EPI PEPERS ITLTIVERAVVALERIEVVEREP VICTOMS ETPHAGA EPI PEPERS ITLTIVERAVVALERIEVVEREVEN VICTOMS ETPHAGA EPI PERS VICTOMS EN PERSONANTI PERSONANTI VICTOMS ETPHAGA EPI RESULTEPHAGA ERAN PROMONIA ETHAGA ES STATUTON ETHAGA EPI RESULTEPHAGA EN PARA EN PERSONANTI PERSONANTI STATUTON ETHAGA ETHAGA ETHAGA ETHAGA EN TAMBA EN EN EN EN EN EN EN EN EN EN EN EN EN
5782	5176	1237	NIMO DESMONHADNYTISYTUTYTEAYMYPLPPEPPIMPPLPPEP PMTPLPPEPPERDEAPPROPALPEDSEASY SYPEPYVOGES LEERAY PTOLOGATAENTYPTEVPELDESEASY SYPEPYVOGES LEERAY PTOLOGATAENTYPTEVPELDESEASY SYPEPYVOGES LEERAY PTOLOGATAENTYPTEVPELDESEASY TAGSTON THE STATE TO THE STATE TO THE STATE THE
5782	5176	1237	NIMO DESAMANADAYTESTIPITEANWPPLPPEPPIMPPLPPEP PPMPPLPPEPPROPAPPED PROGRAPTOSALTAENTMPTEVPELDESESSY SURPEPVÄGES IS EPSAV PYTEVSAS DESVUESSALTVEEP PERESSITATPVERAVAJEBIEVVPERPTTAMS EPTAMSAEPT PERESSITATPVERAVAJEBIEVVPERPTTAMS ETTAMSAEPT PERESSITATPVERAVAJEBIEVOVERPTTAMS ETTAMSAEPT PERESSITATPVERAVAJEBIEVOVERPTTAMS ETTAMSAEPT BESTUTATION OF THE PROGRAM ETTAMSAEPT BESTUTATION OF THE PROGRAM ETTAMSAEPT BESTUTESTAMSAEVEN DES TOTA ETTAMSAEPT LIESSITATPVERAVEN DES TOTA ETTAMSAEPT LIESSITATS ETTAMSAEVEN DES TOTA ETTAMSAEPT LIESSITATS ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMSAEVEN DES TOTA ETTAMASEVEN DE SERVE PERES EN ENTRE EN EN ESCREPTERES EN EN ENTRE PERES EN ENTRE EN EN ENTRE
5782	5176	1237	NIMO DESAMONHADOS YTOS YTOT Y TEA YMYPPLP PETP PYMPPLP PETP PMTPLP PETP PETM ALAP TEGRAL TAENTY PTEV PETP PYMPPLP PET PMTPLP PETP PETM ALAP TEGRAL TAENTY PTEV PETP PYMPPLP PET PMTPL PETM ALAP TEGRAL TAENTY PETP PAT TAENTY PETP PYMPPL PYMPPL PYMPPLP PYMPPL PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPLP PYMPPL PYMPPLP PYMPPL PYMPPLP PYMPPL PYMP
5782	5176	1237	NIMO DESAMANASYTESTIPITETAMYPPLPPEPPIMPPLPPEP PIMPPLPPEPPROPADPAPEDROADPEDSAMANASYTESTIPITETAMYPPLPPEPPEPPROPADPAPEDROADPEDSAMANASYTESTIPITETAMYPPLPPEPPEPPROPADPAPEDROADPEDSAMANASYTESTIPITETAMYPPLPPEPPEPPEPPEPPEPPEPPPEPPPPPPPPPPPPP
5782	5176	1237	NIMO DESAMONHADAS YTES TELTITEA YMYPPLPPEP PYMPPLPPEP PMPPLPPEP BERD AD ALPTEGALTAENTYPTEVPELDESERSY ORDEPVAGES IS BEFAN PTIGS YAS BORDHUSSEN ATVEREP PMPRPLAGES IS BEFAN PTIGS YAS BORDHUSSEN ATVEREP PLAGES PHAGE AND THE SENSE OF THE SENSE
5782	5176	1237	NIMO DESMONNADSYTESTUTYTEAYMYPLPPEPPYMPPLPPEP PMTPPLPPEPP WORD ALP PEOCALTAENTH/TEXPELDESESSY PMTPPLPPEEP WORD ALP PEOCALTAENTH/TEXPELDESESSY PMTPPLPPEEP WORD ALP PEOCALTAENTH/TEXPELDESESSY VERSIESTUT, PMTPPLAN ALP BEBEVER WORD ALP PEOCALTAENTH/VERSITYTY LASEPPYMSETAETEDINADOR WORD ALP PEOCALTESTYTY LESSYMYZEEPVAREDYVITEVPEWALLESSYMYLESSYTVLESSTYTY LESSYMYZEEPVAREDYVITEVPEWALLESSYMYLESSYTVLESSTYTY LESSYMYZEEPVAREDYVITEVPEWALLESSYMYLESSYTVL EDSYMYZEEPVAREDYVITEVPEWALLESSYMYLESSYMYLE LILESSYMSHWYCH IN LISESOORIAN FEI CONGESTALLISEDEEP RESIVESESSYMYLESSYMYLESDY ALB PHALEST LILESSYMSHWYCH IN LISESOORIAN FEI CONGESTALLISEDEEP RESIVESESSYMYLESSYMYLESTALLISEDEEP LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLESTAET LILESSYMSHWYLESSYMYLTISSYMYLESSYMYLESSYMYLTISSYMYLTAENSYMYLESSYMYLESSYMYLTISSYMYLTAENSYMYLTISSYMYLTAENSYMYLTISSYMYLTISSYMYLTAENSYMYLTISSYMYLTAENSYMYLTAENSYMYLTISSYMYLTAENSYMYLTISSYMYLTAENSYMYLTAEN
5782	5176	1237	INTO DESAMONHADSYTESTICITYTANWPPLPPEPPIMPPLPPEP PPMPPLPPEPPEM AD ADTEGRATAENTMYTTEVPELDESTROY ORDSPANGESIS REPAYPTIGSYSSEDSVURSERVYTEEP PPRSSTTLTPVERAVAGEEVVEREPVICTOMS TEPHAGAEPT PPRSSTTLTPVERAVAGEEVVEREPVICTOMS TEPHAGAEPT PPRSSTTLTPVERAVAGEEVVEREPVICTOMS TEPHAGAEPT ESTATEVAGEEVVEREPVICTOMS TEPHAGAEPT PPRSSTTLTPVERAVAGEEVVEREPVICTOMS TEPHAGAEPT ESTATEVAGEEVVEREPVILTEVEREPVILTOMS TEPHAGAEPT ESTATEVAGEEVVEREPVILTEVEREPVILTOMS TEPHAGAEPT ESTATEVAGEEVVEREPVILTOMS TEPHAGAEPT ESTATEVAGEEVVEREPVILTOMS TEPHAGAEPT LIESSIMSSIMKEINISSGORIAAPEICHGETALISTEM LIESSIMSSIMKEINISSGORIAAPEICHGETALISTEM LIESSIMSSIMKEINISGORIAAPEICHGETALISTEM LIESSIMSSIMKEINISGORIAAPEICHGETALISTEM LIESSIMSSIMKEINISGORIAAPEICHGETALISTEM LIESSIMSSIMSTATISTIGLIKKEINISTIGSTIGSTOMS TITTOMS TOPPALEPD LIEGEKLICHSETYGTATISTIGLIKKEINISTIGSTIGSTOMS TITTOMS TOPPALEPD LIEGEKLICHSETYGTATISTIGLIKKEINISTIGSTIGSTOMS TITTOMS TOPPALEPD LIEGEKKINGSISTIANUS PPACALISTEM SETTIME PPYKROLIDO LIEGEKKINGSISTIANUS PPACALISTEM SETTIME PPIKROLIDO LIEGEKKINGSISTIANUS PPACALISTEM SETTIME PPIKROLIDO LIEGEKKINGSISTIANUS PRAGAETTISTIANUS TERMINISTIANUS TOPPALEPD LIEGEKKINGSISTIANUS PRAGAETTISTIANUS TERMINISTIANUS TOPPALEPD LIEGEKKINGSISTIANUS PRAGAETTISTIANUS TERMINISTIANUS TOPPALEPD LIEGEKKINGSISTIANUS PRAGAETTISTIANUS TERMINISTI
5782	5176	1237	NIMO DESSMONHADNYTUSYTUTYTEAYNYPLPPEPPINPPLEPEE PINTPLIPPEEPPENDE ALPTROGALTAENTHYTEYPELDESENSY DESSMONHADNYTUSEPPENDE ALPTROGALTAENTHYTEYPELDESENSY DEPPRYGGES EERSKYPTISYSAADDENIUSENTYTUSEPPINPLEPEEP PINTPLIPPEEPPENDE ALPTROGASTAENTHYTEYPENDE ESSWOYTHEREN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI ESSWOYTHEREN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI ESSWOYTHEREN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI ESSWOYTHEREN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI ESSWOYTHEREN SETTINGEN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI LIESSI THESSWOYNCH IN LIESTOOLITE ALTO SETTINGEN PINTPLIPPENDE ALPTROGASTAENTH SETTYTI SETTYTI LIESSI THESSWOYNCH IN LIESTOOLITE ALTO SETTINGEN PINTPLIPPENDE ALTO SETTINGEN P
5782	5176	1237	NIMO DERROMANADAYTESTILITYTAAWPPLPPEPPIWPPLPPEP PIWPPLPPEPP DEG ALPTEGALTAERTWYPTEVELDESENSY ORGENPAGGES IS ERGAVPTUSSAS DESVURSAS ALVTVEEP PEPERSTILTYVERAVVALEREWVEREPVICWESTPHAGAEPT PEPERSTILTYVERAVVALEREWVEREPVICWESTPHAGAEPT ERGAVETTUSSAS ALVTVEET ALVT
5782	5176	1237	NIMO DESAMONHADAS YTOS YTOTY TEA YMYPPLPPEP PYMPPLPPEP PYMPPLPPEP DEGO ALPTEGRATAENTYPTEVPELDESENSY OPEPPVAGES EERSEN PYTTES YRAS SADDON'USES ALVTYBEP PAGES EERSEN PYTTES YRAS DEGOVERS ALVTYBEP PAGES EERSEN PYTTES YRAS DEGOVERS ALVTYBEP YLASS PYMGETAETTO BOND ALGERYAS YN YSTELLYPPATTYLA ELIGEPYMAE PSANALUSES ANT VILESSTYTYL ESSTYTYL ESSTATYL SETTEM ELIGENY STATES YN YSTELLYPPATTYLA ENGLYSTEPS ALVTYBEPVAGED YN I ENGLYSS ENGLYSS YN YSTELLYPPATTYLA ELIGEPYMEE SHANALUSES ALVTYBE STYTYL ESSTYTYL ESSTATYL SETTEM ELIGENY ENGLYSS ENGLYS
5782	5176	1237	NIMO DERROMANADAYTESTILITYTAAWPPLPPEPPIWPPLPPEP PIWPPLPPEPP DEG ALPTEGALTAERTWYPTEVELDESENSY ORGENPAGGES IS ERGAVPTUSSAS DESVURSAS ALVTVEEP PEPERSTILTYVERAVVALEREWVEREPVICWESTPHAGAEPT PEPERSTILTYVERAVVALEREWVEREPVICWESTPHAGAEPT ERGAVETTUSSAS ALVTVEET ALVT
5782	5176	1237	NIMO DESAMONHADAS YTES TELTITE A WWPPLP PERPEPUMPPLEPEE PPMTPELPERE PERGE ALP PEGGALTAENTHYPTEVPELDESERSY OPERPEVGGETE BEFAN PTICS YAS ABD DEVILUES ALTVE BEP PPMTPELPE PERGE ALP TELGE ALP TELGE ALTVE BEP PPMTPETANT PEGGALTAENTHYPTEVPELDESERSY TLASEPPWGETART PEGGALTAENTH ALTVE BETTEVT LESS THE PMTPETANT PEGGALTAENTH BEST WITH EPSTATTAENTH ALTVE BETTEVT EPSTATT PEGGALTAENTH BEST WITH SECTION THE EPSTATT PEGGALTAENTH BEST WEIGHT ALTVE BETTATT LESS THE STATEMENT
			NIMO DESSMONHARDSYTESTILITYTEANWYPLPFEPEPIMPPLEPEE PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY VILASEPPMSETAETTEGNERALGGANGSEVETSLUPPAUTTEVLA ELIGEPMANERSHAWALESESTYTUSESTYTYLESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELTORYEETALSTYM ILESSITMSHAWCITHISGGORIHAPEINAGETALHEGEEPERAL ENTIVEESESSYETHETHYSETATU
			INTO DESAMONHADSYTESTUTITANWPPLPPEPPIMPPLPPEP PMPPLPPEPPERD ALP PEGALTAENTMYPTEVPELDERENG PMPPLPPEPPERD ALP PEGALTAENTMYPTEVPELDERENG PMPPLSESTER ALP PEGALTAENTMYPTEVPELDERENG PMPPLSESTER ALP PEGALTAENTMETET ALS PEGALTAENTMYTESTEP PRESENTATION AND ALP PEGALTAENTMETET ALP PAGALTET PMPLSESTER ALP PAGATET PMPLSESTER ALP PAGATET PMPLSESTER ALP PAGATET RESENTATION AND ALP PAGATET ESTATION AND ALP PAGATET ESTATION AND ALP PAGATET ESTATION AND ALP PAGATET ESTATION AND ALP PAGATET LLESS LIKESHWIKE IN LISS GOUNTAEPE IN ALE SET PMPLSESTER LLESS LIKESHWIKE IN LISS GOUNTAEPE IN ALE SET PMPLSESTER LLESS LIKESHWIKE IN LISS GOUNTAEPE IN ALE SET PMPLSESTER LIKESTER ALP PAGATET ALS LIKE KINGTHE SET ALP PMPLSESTER LIKESTER ALP PAGATET ALS LIKE KINGTHE SET ALP PMPLSESTER LIKESTER ALP PAGATET ALS LIKE KINGTHE SET ALP PMPLSESTER LIKESTER ALP PAGATET ALS LIKE KINGTHE SET ALP PMPLSESTER ALP PM LAND ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER ALP PMPLSESTER AL
			NIMO DESSMONHARDSYTESTILITYTEANWYPLPFEPEPIMPPLEPEE PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY PMTPELPEEPENDERALPTEGGALTAERTHYPTEYPELESESSY VILASEPPMSETAETTEGNERALGGANGSEVETSLUPPAUTTEVLA ELIGEPMANERSHAWALESESTYTUSESTYTYLESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELESTYTYL ESSVUTYEEPEVALEPTYLTEYPENVELTORYEETALSTYM ILESSITMSHAWCITHISGGORIHAPEINAGETALHEGEEPERAL ENTIVEESESSYETHETHYSETATU

SEQ	Predicted	Predicted and	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Fhenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Iscleucine, K=Lysins,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYI
1	1		GTEPWKPKEAVERNGVITDKADIFAFGLTLWEMMTLSIPHINLS
i			NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE
5784	2669		LFSVCTNEDPKDRPSAAHIVEALETDV
3764	2009	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
			GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
i		1	RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGPDRHRODW
			VDSGCPEESKEKMCENTEPVET\FLEPPOP*ERCPPSSGS*LPP
1			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1	J		HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIRRRPSR
	Į.		WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
			GILSNITHROAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQNDHVHL
1			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
	1		GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
	ł		TPLPTCLOFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
1			VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
i			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
			WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5786	2532	1674	SYKLPAAERRASSCSOPPTPTRRRWPAPGRTSRGHRPQM*SGTP
			APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M
1			S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
			SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP
			SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
1			GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNWNPMMAE
5787	2	2460	MASAASVTSLADBUNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
			T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV
			VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR
1			EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS
1			RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES
1 1	i		QDGDILRQRDBFDLLVAGEICRFSALIEELEEKNERPARELLTD
l i			IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF
1			LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS
			PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
			BDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
1			RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPPPGLNG RGSSFSLSS
5788	2	6860	3HSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG
		****	SEGEGEGETEGDVHTSNRLHMVRLMLLERLLOTLPOLRNVGGVR
1			AIPYMOVILMLTTDLDGEDRKDKGALDNLLSCLIAELGMDKKDV
1			SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSS_CESSSLISS
1 1		[ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP
1 1			HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQT
			KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL
1			FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
1			SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
			FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
			SSPAPVAASSQQATTQSKSSTKKSKKEEKEKEKDGETSGSQEDQ
			LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRNQAHCLTLH
	1		IYRNSSKSOOELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSOKAVEILRTONHILTNHPNSNIYNTLSGLVEF
	1		DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI
1 1			GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
1 1	ł		RWHKAKKVOLTPGOTEVKIDLPLPIVASNIMIRFADFYENYQAS
			TETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDFF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /mpossible nucleotide deletion,
	seque.tee		\=possible nucleotide insertion)
		i	LCNACGFCKYARFDFWLYAKPCCAVDPIENESDRKKAVSNINTL
			LDKADRVYHQLMGHRPQLENLLCXVNEAAPEKPCDDSGTAGGIS
			STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE
1			YDLOQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
ı			CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA AAMREEVRQLMCDLTRDNPEATQQMNDLIIGKVSTALKGHWANP
			DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP
1		1	VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN
			EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH
i i			LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
			QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
		ĺ	YLALYQKLITSAHWKYYLAARGYLPYVGNLITKEIARLLALEEA
			TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
			LCLRKLVVQRTKLIDETQJMLLEMLEDMTTGTESETKAFMAVCI
			ETAKRYNLDDYRTPVFIFERLCSIIYPEENEVTEFFVTLEKDPO
			QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICODCDLVALLED
1	1	ľ	DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
			LLGDATERFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN
			RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
			VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\ICAEPNVEP
l l			LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP
			YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
			IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
l	i		RIWDADI\WKSFCLRPALPFILRLLRGLAIOHPGTOVLIGTDSI
1			PNLHKLEGVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
í	ĺ		RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA
			DWEELIEEP\GLTCCICREGYKFQFTKVLGIYTFTKRVVLGGVW
			ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA
			LQNANTKCNGLLPVWGPHVPESAPATCLARHNTYLQECTGQREP
			TYQLNIHDIKLLPLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
	-		GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
			LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV
			KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
1			HNDMFIYEAADKALKTFOEEFMPVETFSEFLDVAGLLSEITDPE SFLKDLLNSVP
5789	1	2407	
3,05	•	2407	LPLHAVEKIGEFGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
			TBEKEKKEKPKSDKTEEIABEEETVFPKAKQVKKKASPSEVDMN SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
1 1			VTKNEEPSEEEIDAPKPKKKKEKEMNGETREKSPKLKNGFPHP
			ZPDCNPSEAASEESNSEIEQEIPVEQKEG\AFSNFPISEETIKL
			LKGRGVTFLFFIQAKTFHEVYSGKDLIAQARTGTGKTFSFAIPL
1			IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
			SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
1			KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS
1			ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH
1 1			WTQRAAVIGDVIRVYSGHOGRTIIFCETKKEADELSONSAIKOD
1 1			AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD
		1	LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ
1 1			VEQKAGIKFKRIGVPSATEIIKASSKCAIRLLDSVPPTAISHFK
1			QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
		ſ	ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
1 1		ļ	DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGO
1 1			REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSONK
			GQKRSFSKAFGQ
5790	3786	1585	ARRORDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY
1			QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD
1	!	J	KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEE
1	1		DAESEREKKENSCHKWSTGEBYIAVGDFTAQQVGDLTFKKGEI
			LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGOESSEE
1			GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
L			HVSFCYLIVLMRNRMETVEDTKGSETGFRAWNVQSRGRIFLVSK

SEO	Predicted	Predicted end	Tauture 19
ID	beginning	nucleotide	Amino acid segment containing signal peptide
CN:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ivo.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Iscleucine, K=Lysine,
}	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PVLQCINTVDVLTTMGAIPAGFRPSTLSQLLEBGNQFRANYFLQ
	1	i	PELMPSQLAFROLMWDATEGTIRSRFSRISLILTLWSCKMIPLP
			GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWQFKKPKTWTFSP
	ł		QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG
1		1	ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI
1	!		SDB3UGGUTYGALTIELFLNGGTPYEKG1EVDPS1
i i			SRRANGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
			GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFFML
	Į.		LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH
ļ	1		\GCVLPLL/HTPTRLPPFRWAEEETBTARWKVITDFLKQNQENQ
	l		GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
5791	3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH
1	1		GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDOLV
1	l		NRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP
			NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY
			IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL
			DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG
	1		VQIYQFPTDDDTIAKVNAAMKGQLPFAVVGSMDEVKVGNKMVKA
			DOVEMBER OF THE PROPERTY OF TH
	l .		RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL
1	I		YRRCKLEEMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKREE
	1		MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK
1			RRLLEBEI IAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF
1			FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ
			LLIFMEKYFQVQGQYISQSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
1			LARRPKLCL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
	İ		TVNVSVPKKTRNNGTLYAYIFLHHAGVLFWHDGKQVHLVSPLTT
			YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1 1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
1			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
1			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
1			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
			AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
1			
		*	DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
			YAPGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
			IITWPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
5793			BKATRAPHTD
5793	2263	653	AAAAPS PAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
1 1			LARRPKLQL\RHSFTTTRSHLGALNN:DLVLNVEDFDVESKFER
1 1			TVNVSVPKKTRNNGTLYAYIFLEHAGVLPWHDGKQVHLVSPLTT
1 1			YMVPKPEEINLLTGESDTQQ1EADKKPTSALDEPVSHWRPRLAL
1 1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDOLSN
1 1			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
1 1			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
1			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEOTSLLVLVP
1 .1			AGVGAAIBLWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
1			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
1		i	VARCEL PMI DOL PRIMER POLYGON IN DAMA THEORY IN THE
1			YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
1	1		IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
5794	1		EKATRAPHTD
5/94	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
	1	J	KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG
	1)	TKGTRGPPGASGYPGNPGLPGTPGQDGPPGPPGTPGCNGTKGER
1 1	1	J	GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG
1			FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGBKGQM
1 1	1		GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGOKG
1 1			EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
			YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
1 1	ŀ		PGPRGEPGPKGFPGLPGOPGPPGLPVPGOAGAPGFPGERGEKGD
1 1		1	RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP
1 1	1		
		j	GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG
			PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Pherylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
í	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	secuence	Codon, /=possible nucleotide deletion,
	sequence	o o quon co	\=possible nucleotide insertion)
			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
			PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
í	1.		DKGQAGFFGGPGSPCLPGPKGEPGKIVPLPGPPGAEGLPGSPGF
i			PGPQGDRGFFGTFGR\PGL\PGEKGAVG\QPGIGFFGPPGPKGV
			DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
1		ĺ	PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG
			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
1		1	FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGCQGAPGIPGFPG
			SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD
			PGLKGDKGDVGLPGKFGSMDKVYMGSMKGOKGDCGEKGOIGPIG
			RKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
	1		GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGQ
			AGFPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
1		l	TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG
			DKGSKGEVGFPGLAGSPGIPGSKGEQGFMSPPGPQGQPGLPGSP
			GHATEGPKGDRGPQGQPGLPGLPGPMGPPGLPGIDGVKGDKGNP
1			GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF
1	1		QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP
			GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA
			PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
i			VTRHSQTIDDFQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP
			ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI
	j		GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
1			YYANAYSFWLATIERSEMPKKPTPSTLKAGELRTHVSRCQVCMR RT
5795	1192	61	
1	1		STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
1	1		VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
			FAIWTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH
1			ETQPIVEILLKNOPKLIEFLSSFQKERTDDEQFADEKNYLIKQI
1			RDLKKTAP*RALRDSKR
5796	2	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
			FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE
i			RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
			GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
,			LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL
	l		GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
1			NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R
1			EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5797			QHRDPG
3/9/	2	891	PRVRQKTLVDVTLENSNIKDQIRNIQQTYEASMDKLRBKQRQLE
1			VAQVENQLLKMKVESSQEANARVMREMTKKLYSQYEEKLQEEQR
1			KHSAEKEALLEETNSFLKAIERANKKMQAAEISLEEKDQRIGEL
			DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS
			ASLRERIRHLNDMVHCQQKKVKQMVEBIESLKKKLQQKQLLILQ
			LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
5798	644	115	SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
3,30	044	112	KILGSRWKSMSNQEKQPYY3BCARLSKIHLKKYPNYKYKPRPKR
1			TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
			VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT
5799	2679	1435	DGGSLAGNEMINGEDENBMYDDYEDDPKSDYSSENEAPEAVSAN
1	20,7	1433	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVBLQQRAVEYL
ı I			TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGSMEPTPSTVSTPSPSADLIGLRAAPPPAAP
			DACACON I UDURINCO A COCI COMPETA DE COCI-
			PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
			PASAGAGNILLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQILQIGVKSEFRQNLGRMYLFYGN
			PASAGAGNILIVDVFDGPAAQPSIGPTPEEAFLSPG?EDIGPPIP EADBILINKFVCKNNGVLFENQILQIGVKSEFRQNLGRMYLFYGN KISVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
			PASAGAGNILLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQILQIGVKSEFRQNLGRMYLFYGN

SEQ	Predicted	Predicted end	Amino acid segment containing signal pertide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidins, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVBLQQRAVEYL
			TLSSVASTDVLATVLEEMPPPPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
			PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
1	1		EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRNYLFYGN
			KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
			NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
			AAQDFFQRWKQLSLPQQEAQKIFKANHPNDAEVTKAKLLGFGSA LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
ľ			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGBITS:KINRVDPSESLSIRLVGGSETPLVHITT
2301	1 3	1413	QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLROP
1			CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1			OLGIKLVRKVDEPGVFIFNVLDGGVAYRHGOLEENDRVLAINGH
1			DLRYGSPBSAAHLIQASERRVHLVVSROVRORSPDIFOEAGWNS
1			NGSWSPGPGERSNTPKPLHPTITCHEKVVNIOKDPGESLGMTVA
			GGASHREWDLPIYVISVEPGGVISRDGRIKTGD1LLNVDGVELT
			EVSRSEAVALLKRTSSSIVLKALEVKEYEPOEDCSSPAALDSNH
			NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
1			GYEEYNGNKPFFIKSIVEGTPAYNDGRIRGGDTLLAVNGRSTSG
			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1	J		GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV
			ITQRLTR
5803	2234	1299	BAQFGTTAEIYAYREEQDFGIEIVKVKAIGRQRFKVLELRTQSD
			GIQQAKVQILPECVLPSTMSAVQLESLNKCQTFPSKPVSREDQC
			SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
1	1		LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAOCKICA
	i		SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
			PCF .
5804	2	1707	BMEKQRQEBORKRTEBERKRRIEQDWLEKRKIQRELAKRAEQIE
			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
			RBEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
			ARROMVNEDBENODTAKI FKGYRPGKLKLSFEEMERORREDEKR
1			KAEEBARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
1			GKLEINFEELLKQKMEEEKRRTEEERKHKLENEKQEFEQLRQEM
1			GREKEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS
1			EKEIQKKIEEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS
			EAPFTHKVNMKARFEQMAKARESEEQRRISEQKLLRMQFEQRSI
			DAALOKKREEEEEEGSIMMGSTAEDEECTRSGAPWFKKPLKNT SVVDSEPVRFTVKVTGEPKPEITWWFEGEILODGEDYGYIERGE
			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLABHASS
	1	.,,	AFKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
			YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNBYKLA
			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
			RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
			ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
1			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
			RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
1			PRGQRTNAQKYCQPCTBSPELYDWLYLGFMAMLPLVLHWFFIEW
			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
L			LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
NO:	nucleotide	location	(A-Alanine, C-Cysteine, D-Aspartic Acid, E- Glutamic Acid, F-Phenylalanine, G-Glycine,
	location		Grucamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first		L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
	į.	I	GLLYYAFPYIILVLSLVTLAVYMSASEIENCYDLLVRKKRLIVL
1	1	ł.	FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
1			EPSRILSEGANGE
S808	2	433	SLPDSGVVEYLSKGGVADNHKDFGELRYNECLUNFSCNGKNGSS
3000	1 4	433	
1			BGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
1			IGVIGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
			LVNGVHLPNRR
8809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
Į.	J	J.	RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
			EVPDGYIIGNYTSSLGSOVRYACREGFFSVPEDTVSSCTGLGTW
			ESPKLHCQBINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
		ı	SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWO
		!	INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC
1	1	i	LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
1			
1			SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
1	1	l	FTTREQVPVVCLDLYPTTDYTVNVTLLRSPXRHSVQITIATPPA
1	ſ		VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF
1	l		AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
1 .	l		TTQITEPPLPEVEFFTVHRGFLPRLRLRKAKEKN3PISSYQVIA
1			LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
			BIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
	l		WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
	l		EIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAOSFRE
i	1	í	VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
1			SFEEINERLLSAMESTASLEKNPAAFSLFEHYDDSSARSDOMLK
1			
1			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
1			EPQDDQEVNELVEEYRLTVKESYCIF3DLEPDRCYQVWVMAVNF
1			TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
1			TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
1			RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
1			SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
1			SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
1			VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
1			KCTLHLGIBPPDSVRHK
S811	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
			WDIEGAVERYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPBLA
1 1			HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
1			
1			RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
1			WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE
1			VYKAVAAVQKSABELASGHLASAFVASQEAVTSSELAFFDPSLL
			HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
			KTD
5812	S204	2744	GGRORCORGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
1 1			LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLOGSGO
1			DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA
1			YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEERE
1			GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ
1			YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
1			DE DE LE LEMACORA AUCTORIA PER CONCERNA AUCT
1			RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
1			LALGYVSSSVLAAAKCDSNTMTPGPWLGLPAVPAVTLYKHDDPA
1	J		LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS
			QRIQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVFASGLTVMDLEA
	1		EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
			3EFKQEVRATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ
1			GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
			AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS
		j	EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			TEPTYVYKAQGAGVTLPFTPSGSRTKQRLPGQKPFKRSLRGSDA
			LSKTSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
			TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERFLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
	1		LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHOI
1	ĺ		GCQSSISGDTGVIHVVEK3EDLQWVLTDGPNPPYMVLLESKHFT
			RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
1	l .		SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
			KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
			SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
1			ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
1	ļ		PRNYMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
1			GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
1			LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
1			ILQGRDLRSYLG*RGLFQH\YIAV\SSPINTIYV/VLQYALANL
1			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
			RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
5814	8500	432	VSY
2614	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
1			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
			AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
			GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM
			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
1			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGOVGGFI
			NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
1 1	'		AKYMKNTPYVNEVSTDBALLKRYRKEIMDLKKQLEEVSLETRAQ
			AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLOGEL
			KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
			LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN
			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
			KDQBMQLIHBISNLKNLVKHREVYNQDLENELSSKVELLREKED
			QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
1 1			ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYOSOLE
1 1			AKKKMQVDLEKELQSAFNEITKLTSLIDGXVPKDLLCNLELEGK
			ITDLQKELNKKVEENRATRRRVILLSELKSLPSEVERLRKEIQD
			KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
1 1			SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE
1 1			AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE
1			NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
1			QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS
1 1		J	KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
1 /	I	J	TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
			KENIEMTIENOEELRLIGDELKKQQEIVAQEKNHAIKKEGELSR
1 1	1	1	TCDRLARVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIB NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
1			KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
1			TIDELRRSVSEKTAQIINTQDLEKSHTKLQESIPVLHEEQELLP
1 1	1		NVKKVSETQETMNBLELLTEQSTTKDSTTLARIEMERLRLNEKF
1 1	1		QESQEEIKSLTKERDNLKTIKRALEVKHDOLKEHIRETLAKIOE
	I		SQSKQKQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
1	I		LSKRLQESHDEMKSVAKEKDDLQRLOEVLOSESDOLKENIKEIV
	i		AKHLETEELKVAHCCLKEQERTINELRVNLSEKETEISTIOKO
			LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR
			KAKDSALQSIRSKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA
		1	LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE
			IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
		J	DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH

SEQ	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	S-Serine, 1-Inteonine, vavarine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
L_	sequence		\=possible nucleotide insertion)
			QETICKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
		i	IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
			TOST KAMERIOL THE VECTOR PROPERTY AND A WAR TO SEE A SEE
]			IQBLKANEHQLITLKKDVNETQKKVSEMEQLKKÇIKDQSLTLSK
i	l		LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLK
	Į.	I	BSLQETKARDLBIQQELKTARMLSKEHKETVDKLREKISEKTIQ
	i		ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
			EMEQLKKQFEPNYLCKCEMDNFOLTKKLHESLEEIRIVAKERDE
		l	LRRIKESLKM3RDQF:ATLREMIARDRQNHQVKPEKRLLSDGQQ
1		l	THE MEGI DEPOSIT AND A PROPERTY OF THE PROPERT
1			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
	I		RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVEKQKELLIK
			IQHLQQDCDVPSRBLRDLKLNQNMDLHIEEILKDFSESEFPSIK
1			TEFQQVLSNRKEMTQFLBEWLNTRFDIEKLKNGIQKENDRICQV
1	į.	l	NNFFNNRIJAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
1	1	1	KNYQTLKTSLASGAQVNPTTODNKNPHVTSRATOLTTEKIRELE
1	1	1	
1	1		NSLHEAKESAMHKESKIIKMCKELEVTNDIIAKLQAKVHESNKC
1	1		LEKTKETIQVLQDKVALGAKPYKEEIEDLKNKLGKIDLEKMKNA
1	l .	1	KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
	1		DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQON
1	1		EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
1			SPKVTGTASKKKQITPSQCKERNLQDPVFKESPKSCFFDSRSKS
1			LDCDUDUDUDUCCI CI CDCUCONA CA BOURGOD) CDUARA DOCUM
1			LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
5815	23		DVP\ECKTQ
2812	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
	l i		VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
	i i		SFVHGVTVKMRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
			QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
			WHICH AND AND AND AND AND AND AND AND AND AND
			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
			SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
			AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
			NEKNKLEMNKVQVDAHGNILLSTLE IRNETSGSEVLTSVSDPKA
1			TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
1 1	1		QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSOAPGAOPSPP
		151	
1			TVYHERQRLELCAVHALNNVLQQQLFSQEAADEICKRLAPDSRL
	1		NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
			VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
1	l l		K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
	l l		SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSFPAAD
1		**0	TIMENTOTION NO MEDICALIZATION OF THE THE LINE
1			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
1 1			KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
1 1			RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
1 1			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
1 1			HPQALMGRGFFSGMAAAGRHLCFL
5818	3	3918	QALRDELWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
1	- 1	9310	
1			DRREGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
1 1			TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
1 1	1		TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
, I		į	PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
1 1	1		NOTENTIAL CONTROL OF C
1 1		J	NGTSNKKSIHEQDTNVNNSVLEKVSGKGCSEPVPQAILKKRGTS
		ļ	NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
1 /			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
	1	J	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
1 1	1		DVRDNKNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
1 1			PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
1 1	ĺ		
1 1			HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
		I	NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCV3DVS
			LCNPERTMGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
F	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
-	sequence		ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
1	1		WNLSTGVLHQRESPESDTGSATTSSDCIKPRSEDYDAGGSODDD
			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
			MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
			GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
i			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
	ļ.		CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1 .	1		SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESKSTTTEK
1			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
1			KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
			PEDLSLAQYLINGTLLLARDSSKPQGITHIDTLNRWSELTSPLD
F010			SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLEGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
1			LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
1			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
			RLRPFLGARVTVNSSFSPIINIHNPHSEFLQVVEMYSSGGDIHL
			ELPTGOOGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
1 1			TNASDSTEFILEPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV
1 1			LNIHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
1 1			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
1			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
1 1			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
1			NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
1 1			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1 1			DGAIQITTDYELTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
1 1	i		VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
			KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
			TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
1 1			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
l i			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
{			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGOLOIHIETIE
			ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
1 1			ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
1			ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD
			VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
			GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
			SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS PLEQHPQPPLPPPVPOPOEPOPERLSPAPLAHPSHPERASSARH
l i			SSEDSDITSLIEAMDKDFDHHDSPALEVFTEOPPSPLPKSKGKG
1 1			KPLQRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
			TSNPDTEPLLKEDTEKOKGKONMPEKHES EMSQVKQKSKKLINI
1 1			KKBIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
	1		SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
	1		PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
	1		PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
	1		SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
	1	ļ	HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
1			VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS
	I		SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
		ĺ	TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
5820	310	1000	RSSDPWSNSHFPHEN
3620		1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIO
		1	and the second state of the second se
i !		i	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRE/DSKALAEFBEKMN
			SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN ENWKKRLEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSS\ SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSESSMSETES

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid sequence	sequence	Codon, /=possible nucleotide de_etion,
_	sequence		\=possible nucleotide insertion)
		i	DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
1	Į		ESEYIZEVRAKKKSSEEREKATEKTKKKKKKKKKKKKKKKKKKAA
			SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF GIIPGLFSSHSDATV
5821	179	915	
3021	1/3	315	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
			PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
1			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\ SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
			RWKEASHRNQLRYSESMKILREMYERO
5822	464	4379	QTLKEMPIVMARDLERTASSSEDBEVISQEDHPCIMWTGGCRRI
5522	***	4373	PVLVFHADAILTKONNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
			LTRKDRLYKNIIRMQHTHGFKAFEILPQTFLLPAEYAEFCNSYS
l l			KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
			LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
1			NIRNOFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
į.		ł	LKQBGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
			FELYGFDVLIDST_KPWLLEVNLSPSLACDAPLDLKIKASMISD
1	i		MFTVVGFVCQDPAQRASTRPIYPTFESSRRNFFQKPQRCRPLSA
			SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
		Ì	RGGFIRIPPTSETWEIYGSYLEHKTSMNYMLATRLFODRMTADG
			APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP
i			KYPVITQPAEMNVKTETESEEBEEVALDNEDEEQEASQEESAGF
			LRENGAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETOR
		1	LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
			QTFSASWAAKEDEQMELVVRFLKRASNNLOHSLRMVLPSRRLAL
			LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
			ENFQEFIRQASEAELEEVLTFYTQKNKSASVFLGTHSKISKNNN
		ĺ	NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA
			EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
			LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
			RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
1			GIAKTOKEGEDASLYSKRYNOSMVTABLORLARKQAARQYSPSS
			HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
			SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
1	l .		VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
5823			:TSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDBPSACRAGDVNMDDPKKEDILLLADEKFDF
	l		DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1	1		TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
			DSPLIGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
]			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
			EIPASFSRTKIPABKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
1			CTPQFVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
1			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
1			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPHTPKTMPRAVGS
1			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1 1			GSPPSRVPQALMFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1 1			BALLVDIKLEPLAVTPDAASQPLIDLPLIDPCDTPEAHVAVGSE
1			SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
			ENVDSPLLKP
5824	42	2293	LLTALSMEGGGGREBPSACRAGDVNMDDPKKEDILLLADEKFDF
		*****	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNOAAOAAKP
			TOTAL TOTAL

NO: nuc	dicted inning leotide ation responding	Predicted and nucleotide location corresponding	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Fhenylalanine, G=Glycine,
NO: nuc	leotide ation responding	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
loc	ation responding		Glutamic Acid. FaPhenylalanine C-Cl
to	responding		GEGIYCINE,
to			H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	no acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	idue of	amino acid	Warrantophan Varunging V Malance
	no acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	uence	boquonee	\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKENKKSPTSLKRRTYYLS
			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
			EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGOGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LORKSSSGA\VWSGASSA
			CTPOPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTOPOTPE
			GGG\QWLMSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1 1			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
i l			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
			SRPLIDLMINTPDMNKNVAKPSPVVGOLIDLSSPLIOLSPEADK
1 1			ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKORSRLSAPGMUH.
			SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL
1 1			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONCS
1 1			VLPGGVYVSETQNRVIILMLTNOTVHRLLLPHPSRMYRSELVVD
			SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
			GEALFALFCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
			GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRNWS YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
1 1			GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
1 1			ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
1 1			EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
1 1			DLSWSELKKEVTLAVENELQGSVTEYEFSOERFRNLOORFWCKF
			YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
			HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
			DMSVIMEMSCYNLQSPEKAABQILEDMITIDVENVMEDICSKLQ
1	1		EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
			GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
	J		TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATOVPLDTLESN
			LOHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
			FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
1 1 .			BCFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
			VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
1 1	ſ		\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
1 1		i	YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
1			TVMFBYGMRLGREVRTLRGLEKOGNCYLAALNCLRLIRPRYAWI
			VQPVSGAVYDRPGASPKRNHDGECTAAPTNROIEILELEDLEKE
			CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS
			LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQAEAWAWLAANQLS
			SVITTKESSATDRAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
5826	3	871	VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
	,	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
	- 1	1	AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQABLAW WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPCGQHG
	- 1		WSKILDVHERDCPWDCASCSAPGLIGCWDQARGLLGPGPGGGGHG CREQLELFQTPGSCYPAQFLSPGPQPHDSPSLLQCPLPSLSLGP
			AVVAEPPVOLSPSPLLFASHTGSSIQGSSSKLSALQPSLTAQTA
1 1		1	PPOPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
		- 1	WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
	ĺ		RENBDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
1 1			RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
			SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
1 1			EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
1 1			SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
			TLKSEREKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

SEQ ID NO:	Predicted beginning mucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first arino acid residue of amino acid sequence	Jamino acid segment containing signal peptidg A-Alanine, C-Cysteine, DeAspartic Acid, E- Glutamic Acid, F-Phemylalanine, GeOlycine, H-Hilbitdine, I-Isoleucine, K-Hywine, L-S-Gucine, M-Mcchionine, NeApparagine, P-Froline, C-Golumanne, R-Arginine, S-Serine, T-Thronine, V-Waline, S-Serine, T-Thronine, V-Waline, S-Serine, T-Thronine, N-Thronon, *-Stop Codon, /-possible nucleotide deletion, L-possible nucleotide insertion) VAVIESTEY/LGPKCHAGGETYCLISPAT/SSKYPPULDUP VAVIESTEY/LGPKCHAGGETYCLISPAT/SSKYPPULDUP VAVIESTEY/LGPKCHAGGETYCLISPAT/SSKYPPULDUP NTSDSIVAITHISLAWIVELIGZEVWGGGRTKIFFETTA)SF NTWITDLESGEDPSGPKTFTHISLAWIVELIGZEVWGGGRTKIFFETTA)SF NTWITDLESGEDPSGPKTFTHISLAWIVELIGZEVWGGGRTKIFFETTA)SF NTWITDLESGEDPSGPKTFTHISLAWIVELIGZEVWGGGRTKIFFETTA)SF
5828	2		SEEMPDMSGPE\SPERNQTVNI\QIMP\REP\CDDVKSGCTILDV EESSWHDCZESSIDTKVNPOGGITATKPYTEGEQKE\PIALIDV EESSWHDCZESSIDTKVNPOGGITATKPYTEGEQKE\PIALIDV EESSWHACSID\QKSID\QKSUDADADDIFPK\SGQRF\PIX\PFEIL GIGEBTIQVKKE\PVKDFWDMFADM\PIS\GKSAFIL\GKSAFIL\GKST EMYPKKDDVS\PVWO\FSSK\FAAAEITBGEA\GKBEGEL\N\VEIN\N W
		257	ARRGSIGAVANCOELS YSCOPCDRAPHISK/TEYVONEFCANV NAVGGGSRITUTUSIS TPPKILIPVONELINIYYDLIKEVGEFCANV LVVTTRIVÇKALCABFRAKKEDIVCIPDDADMATADSLKYITY KLYTUTVILSCOLITOVALHEVYDLIFARVDSIALMARKGCDSI EPVFGCKKKKKAVEQABFIGVDSTGKRILIFAKEADLDBELVIK SCLICHHEPLETFIGUNDALIKUKKKYIVDFILMENSY SITEIRS ELILFYLV/RGKGPSSASSQCTFKKKEGGGKKKKGLKSFRISY STYKERAKYTGABPYONACH
5829	260	. 1259	POCRLIVSCEBENTITATIONTHINGCONNESSAVERNETOPINES OTCLASASSOVOTAVIDVANUALICAMICVASVOTAVIDATIONS YLLTASSOTILATIOLAGINETYPOOPTIVS SEAGRAT YLLTASSOTILATIOLAGINETYPOOPTIVS SEAGRAT ASGRATOTOLARINTEDELINGGRIKTRINKRINGENESPHILDIT PETTPHHEBRYETVEDFITALIDALIOSIA*S SICRELLEPLINTSF PETTPHHEBRYETVEDFITALIDALIOSIA*S SICRELLEPLINTSF CRITTATIONAGENESSAVERY CRITTATIONAGENESSAVERY CRITTATIONAGENESSAVERY TUTTSPUKUKUKUKUKUKUKUKUKUKUKUKUKUKUKUKUKUKUK
5830	4496	3139	GGENALPERENDITECTS RELIGIPOUTUIESENGCERTIEGUNS MIEAAVODRIANGEGESTEVENTSPERICHTVANDET YSTYVES POPRGLIGMSTYLLIMLPS RTYTTILDIERSKLEPINGSTYLLIMENTE POPRGLIGMSTYLLIMLPS RTYTTILDIERSKLEPINGSTYLLIMENTE LVYLIMGDONGLOSSEVENTLONPOVISLINTRALLSWLGSTYLCES LVYLIMGDONGLOSSEVENTLONPOVISLINTRALLSWLGSTYLCES LVYLIMGDONGLOSSEVENTLONPOVISLINTRALLSWLGSTYLCES LVYLIMGONGLOSSEVENTLONPOVISLINTRALLSWLGSTYLLIMENTE LADGEREKKERESSERSKERVGENOONLAGERERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDESVENTIERKLIMENDEVERSERGOUTUREKERK LEGLEPERSPONDENSVENTERGOUTUREKERK
5831	71	3897	FOSKUKCLTYLIPS INNS KSCYAK PRANSOPRIAVMESERGYWZ DOD ISBYRES INDS VILOVOS SENS DISBYRHES SOP SPELDS FOGRSKOTTE POVI LINGS SED GREGS DISBYRHES SOP SPELDS FOGRSKOTTE POVI LINGS SED GREGS DISBYRHES POVI KNOWS ARTISIGARE PRANSOPRIA LINGS AND SENS DISBYRHES POVI KNOWS EARLY SENS SENS SENS SENS SENS SENS SENS SEN
5832	2454	829	NGLLNCNDCYMRSRSAGQPTTL PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN SENLBKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEO	Predicted	I W. 17	
ID		Predicted end	Amino acid segment containing signal peptide
No:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1		to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion}
i		1	VPOGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
			RVHFHLPYRWQFLDRGKWEDLDNMELIBEAYCNPKIERILCSES
		1	ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
Į.	1	l	PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
1	1		QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
	ŀ		YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYOWOKGQMQKQNG
1			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
1			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
			TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWBGMRKHLHT
1			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
1	1		GROWNVKWEENLLHAVAKNYTLLQTIPFFERPFKDHCVCLEWNM
			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
			RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
			EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
1	i e		GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
			PSNCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
1			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
1			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1			YPLDWELSYAYYSNIATKTPLDQHTLQGEQAYVETIRLKDDEIL
1			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQNLFWGQQGVAKNP
1			EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
1	ì		KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EB\MGN
			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
			WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
	1		AYLEGSWHEALLYYVLAABTGIEVSQTNLAHICEERPDLARRYL
			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
			VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDST_H
i			SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
			SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
			STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGATPASPSDSLGOGNSOGPPRTPKPPRT/OECG
1			SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
1			NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI
			PQVKCNEQPNRVEIYEKTVEVLBPEVTKLMNFMYFQRNAIERFC
1			GEVERLCHAEREKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
			KNDHSAYKRAAQFLRKMADPQSICESQNLSMFLANHNKITQSLQ
			QQLEVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
1			GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKCLQVVPLFGDMQI
			BLARYIKTSAHYBENKSRWTCTSSGSSPQYNICEQMIQIREDHM
1			RFISELARYSNSEVVTGSGRQEACKTDAEYRKLFDLALQGLQLL
			SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALODFSO
			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
			RGEKDPKSG*DIKVPRRAVGPSSTOLYMVRTMLESLIADKSGSK
			KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL
			WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL
			YSLDLYNDSAHYALTRFNKQFLYDEIBABVNLCFDQFVYKLADQ
			IFAYYEVMAGSLLLDKRLRSECKNOGATIHLPPSNRYETLLKOR
			HVOLLGRSIDLNRLITORVSAAMYKSLELAIGRFESEDLTSIVE
			LDGLLEINRMTHKLLSRYLTLDGFDANFREANHNVSAPYGRITL
			HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP
			QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
			MRELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
			EFFHHOLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
			EVCDLLHAAPFQNILPRVHVKEGERLDAKNKRLESKYAPLHLVP
			PACEDINAME TO THE PROPERTY OF

SBO	Predicted	[No. 32 at a 3 am 3	I had a second a seco
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	
i	corresponding	to first	H=Fistidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bedacine	\=possible nucleotide insertion)
-	boquoneo		LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1			DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
ł	1	l	EQCFGDGLHWAGCMIIVLLGOORRFAVLDFCYHLLKVOKIDGKD
			BIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGBGTPVE
		Į.	HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPBVPBVVVSRCMLQNNNNL
			DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLO
			SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFCOEPO
			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSOOT
			PRENPINVTLAPNICTGRNTPTSLHIHGVPPEVLNSPOGNSIYI
ĺ			RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
			PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
			SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR
			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDEIMSRSQPKVYISA
			NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
1			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
İ			GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
1			LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
1			QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
			KARMERLQRELEIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
			HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
			CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
1			SDVNYQCLFSAHVLHLRGVLTTQPVBDBRGNVFLWNGBIFSGIK
1			VEAEENDTQILFNYLSSCKNESEILSLFS3VQGPWSFIYYQASS
1			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
1			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA* VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
1			FPMCHLQERYFKSFLLMYT*KEVIQOFIDVLSVAVKKRVLCLPR
	ļ.		DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
1			PIDLINVAFIABEKTMPTTFNREGNKOKNKCEIPSEEFSKDVAA
	١.		AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
į.			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
l			VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
			MELGRISSRNLGRODRVIGDHGKEARFPFLDENVVSFLNSLPIW
			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
1			KMEKINEKASDKCGRLQIMSLENLSIBKBTKL
5837	4792	903	NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
1			KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGBLLQWDLT
			QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
1			RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
			MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKBGCLAFGT
			DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
i .			GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
			KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLCTIQQH
1			HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
1			P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
1 1			VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
			DPDCIYSG\ADDFCVHKWLTSMQD:SRPPQGKKSIELEKKRLSQ
			PKAKPKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ
			EGESQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHODCL
			VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDI3GKG
			HLENGHPELFHOLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
			GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYBAVELLKS
			NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
			CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
			LRCAOELLLANNWVGAOEALQLHESLQGQRLVFCLLELLSRHLE
1 1			
			EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY QEAFOKLQNIKYPSATNNTPAKQLLHICHDLTLAVLSQQMASW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /mpossible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD HQSPATPAFKSLEAFFLYGRLYEFWWSLSRFCPNSSVWVRAGHR
i		i	TLSVE?SQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
1		Į.	LSTFKELFSEKHASLONSORTVAEVOETLAEMIROHOKSOLCKS
			TANGPOKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
1		1	ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
			QAQEL-QKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPACRDLYRDVMLENYSNL
			ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
			LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH
			RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
			IHTNEKPYQCNACHKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
			FSYCSQYTLHQRIHSGEKFYECKDCGKAFILGSQLTYHQRIHSG
			EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
1	1		SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
			KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
			EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLNLTILSEHQ
			RIERGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
			GRAFSRGSEHTLHORIHTGEKPYTCVCCGKDFRCPSOLTOHTRL
			HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLFLRGRRQDGRWTVDFEECLKD\SPRFRAAL
			EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
1	ŀ		RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
			EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
			PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGJA
			AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
			HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
			AYREKDDESEKLDKKSSFSTGSLDSGNESKEKLLKGESALORVO
			CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
			VRSLTLDTWEFBLLKLMCELGNDVINRVYEANVEKMGIKKPQPG
İ			QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
1			EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
			TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
			AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
1			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEEGKDP
1			LSIAVEAANADIVTLLELARMNEEMRESEGLYGOPGDETYODIF RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLNQISSPRWRSEQRAFMSALSKTQTQSAFALQ
1 -540		5520	GLSSLLQSVTGNFVPASEAASQSTSASPANTTVYTIKGRNLPSS
1			AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLF
			SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHFSDFQ
1			RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
1			SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
1			SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
1			PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
1			KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
1 .			SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
	- 0		LFSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
			RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY RIETRVSSSCLDLPDSTERKGAPIETLGYHSASNRRMSGEPIQT
			VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
			SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
			LPPSPLEHGTPFOREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
			VDLSNPFTKEAALAHAAPPPPPPGEHSGIPFPTPPPPPPPPGEHSS
			SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
L			KDHSSLLQGTLARHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amine acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDT1SRSGIT
1	j		LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF PPRY
5841	1908	762	
5042	1,500	762	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
1			TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSPP
1			GDGLDSGLARRGSAVSALASGLVERPMLGPPFHPTPRFKAVSAK
			SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
	1		QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
1			\VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHI
1	1	1	FP+GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
	Į.		LGHCYRGPSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
1			WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
			HRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
			RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLCPQEA\EG
			KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLOPSS
1			RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
			RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
			GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
1			DPRHLVFIDNKGFFDRSEDNLMFKLLEGIKEFPASAVYVLKSQH
			LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
1			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
i			DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA
1			BEARCPVSAPHEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
1			LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
			LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
1 1			LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG
			VQARAPGLGRA
5844	202	2471	PDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
			KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
			QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
			PRGEPGPRGPFGPPGLPGHGIPGIKGKPGPCGYPGVGKPGMPGM
			PGKPGAMGMPGAKGEIGQKGRIGPMGIP*PQGPPGPHGLPGIGK
1 1	1	ı	PGGPGLPGQPGPKGDRGPKGLPGPQCLRGPKGDKGPGMPGAPGV
			GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPOQPGFPGGKGEQGL
1 1			PGLPGPPGLPGIGKPGFPGPKGDR3MGGVPGALGPRGEKGPIGA
			PGIGGPPGEPGLPGPGPPGPRGPPGAIGFPGPKGEGGIVGPQGPPG
1 1			PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP
1			GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
1 1	1		PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPOGOPGL
1	- 1	1	PGPPGPPGPPAVMPPTPPPQGEYLPDMGLGILGVKPPHAYG
	· 1		AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
1 !			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
	I		EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVES
5845			SFSGYLLYPM
2842	215	2061	HASNKSASLQDKMANDKEKTAMCLVNELARFNRVQPQYKLLNER
	ĺ		GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
]]	J	1	KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
		1	PFPNNRANYNPQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT
1 1	ſ		RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS
1		1	BISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
		1	GEGNSKKLSKKRAATTVLQELKKLPPLPVVEXPK\HPPKKRPKT
		- 1	IVKAGPEYGQGMNFISRLAQIQQAKKEKEPDYVLLSERGMPRRR EFVMQVKVGNEVATGTGPMKKIAKKNAAEAMLLOLGYKASTNLO
1 1		i	DQLEKTGRNKGWSGPKPGFPEPTNNTPKGILHLSPDVYORMEAS

	Predicted	Predicted end			
SEQ			Amino acid segment containing signal peptide		
:CN	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,		
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,		
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.		
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,		
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,		
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop		
	amino acid	sequence	Codon, /=possible nucleotide deletion,		
i	sequence		\=possible nucleotide insertion)		
			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM		
		1	NGTSSTABAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC		
1	J.	I	DROSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC		
1	1	1	YGPARKWKAIKMBAMCAHAALLSLIHYLLAPSARLEKSKLFALG		
			N.		
5846	1126	456			
2010	1120	436	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF		
	1	1	KPESEIETDKNGFLQYDVLBALNMEKMMSAISCWMESARHSVVS		
			TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPY3ECKR		
1	Į.		RRSTRVYQPPDSFGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT		
1		1	KSEEDLFLQVYEELIQELAKQKCLQVTA*RRNTTNPS/CK*IRK		
	1	[IQGVI		
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTORE		
i	I		WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE		
1			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK		
1			HKRDDSWSSNLLESWEYEGSLERQQANQCTLPKEIKVTEKTIPS		
1	1		WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK		
i	ì	1	KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF		
			CDCCAL TAHOD THEODER T		
	1		SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE		
1			KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG		
i			HFNEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK		
			CNECGKAFNGPSTFIRHHMIHTGBKPYECNECGKAFSQHSNLTQ		
I	1		HQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC		
			GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT		
J	l .		HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF		
			SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHLTOHKRIHTGA		
			KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS		
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK		
			CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N		
1	J		KHORLHPGT		
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK		
	1		GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL		
1 1			DGYSKKKYVCKLLFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG		
1			VI. PTOWN INCOMES THE TWO PERSONS ASSESSMENT TO THE PERSON OF THE PERSON		
			YLFISVLVNSKSELIRLINNAIKNDLASRNPTFMGLALHCIASV		
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			YLFISVLVNSKSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLMDQHLGVVTAATSLITTLAOKNPBEFKTSV		
			YLFISYLYNSKSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGTHDSYKQSAALCLLRLYRTSPDL YPMGDMYSRVVHLLHDQHLGVYTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFIGLSVKLLRLLQCY		
			YLFISYLVNSNSELIFLINNAIKNDLASRNTTPNGLALFCTASV GSRENALBAFAGEI PKVLVAGOTYDGSVKGSALCLLELY TETS PDL VFMGDWTSRVVHLLINDQHLGVVTAATSLITTLAQKNDEEFKTSV SKAVENSKASTOLOGYTTYFECGETGLSVKLLKRLQCY PPPDPAVRGRITECLETILNKAGEPPKSKKYONSNAKMAULFERA		
			YLFISVLWISNSELIRLINNAINDLASRIPTFMGLALRICIASV GSREMARAFROĞI PKVLVAGĞĞI KYLVLAĞĞI İNDÜNGÜNÇA KÜLTÜLRI YRTİSDÜL VPMODUTSKVUHLANDOHLOVUTAATSLITTLAÇKIN PEFKTSV VPMODUTSKVUHLANDOHLOVUTAATSLITTLAÇKIN PEFKTSV VPMODUTSKVUHLANDOHLOVUTAATSLITTLAÇKIN PEFKTSV PPPDPAVAGRUTECLETILIN KODEPINSK KVOHSINAN NAVLFERA BLIHHDISSPHLIVRAC KONGOFICH PETRIN VIALISHMICTLA		
			YLFISYLVANSKSELIRLINNAINDLASRIPTFMGLALECIASY GSREMBABAGES PYKUVAGOPDOSYGGAALCIALFYRTSDI. YPMGDMTSKVHLLINDGHLGVYFAATSLITTLAGINPBEKTSY SLAVSRLS\RIVYSASTDLQDYTY-FGOFIGLSVKLLINLOCY PPPDFAVRGRITECLETILMTGGEPPKSKKYGISHAKMAVHFEA. ISLIIHDSEBNILVRACKQLGGFLGRETMLKYLALESMCTLA SSEFSHEAKVHLTEYVINLAKTERDVSYGRGAVDLIAMCKDEN		
			YLFISYLMENSELIPLLINALIGILASHNYTHOGALHCIASY GSREMAEAFAGE IFWLVAGOTDHOWSGOSALCHLIAVERSDI. OFROMEAFAGE IFWLVAGOTDHOWSGOSALCHLIAVERSDI. OFROMEAFAGE IFWLVAGOTDHOWSGOSALCHLIAVERSDI. OFROMEAFAGELITELAGE IFWLOGATHOWSGOSALCHLIAGE PPPDPAVAGRITHCLETTLINAGOEPPESKYCHISHNONAULERA SERFSHEAVEHIETVINALUTERUSVEGGANDHAMACDESH APQUVARMESTERADISTERETURVALUTERUSVEGGANDHAMACDESH APQUVARMESTERADISTERETURVALUTERUSVEGGANDHAMACDESH		
			YETSUMINSESELIPLLINALIGILASENTHOMALICIASY SERMADEAFAGE PRIVALAGOTHOMAGSAALCHAUPERSDL VAMODIFSEVULLINDENGOVERATELITIAGENESERTSV VAMODIFSEVULLINDENGOVERATELITIAGENESERTSV VAMODIAGANINASERTOLOGOPPESSEVUNDENGOMALIERA LIGHT LINDENGOVERATELITIAGENESERTSV SERSIELEN VALLEN VA		
			YLFISTUMENSELIPLLINALIGILASENITTHGIALICIASY GERMALEAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGELITELITAGAGEPPESSKYGHSINGAALEEA SLAWSLAS ILVINASATGLOOTTI-THGAGEPPESSKYGHSINGAALEEA SLAWSLAS ILVINASATGLOOTTI-THGAGEPPESSKYGHSINGAALEEA SEFFSHEAWKHISTVINALITERDISVEGENOMI-THAGAGEPSST-THAGAGEPST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGETST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGETS-THAGAGETS-T		
			YLFISTUMENSELIPLLINALIGILASENITTHGIALICIASY GERMALEAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGE IFWILWAGOTHGWASGAALCHLEVIETSDI OFROMERAFAGELITELITAGAGEPPESSKYGHSINGAALEEA SLAWSLAS ILVINASATGLOOTTI-THGAGEPPESSKYGHSINGAALEEA SLAWSLAS ILVINASATGLOOTTI-THGAGEPPESSKYGHSINGAALEEA SEFFSHEAWKHISTVINALITERDISVEGENOMI-THAGAGEPSST-THAGAGEPST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGETST-THAGAGEPTST-THAGAGEPTST-THAGAGEPTST-THAGAGETS-THAGAGETS-T		
			YEFISYUNMANSELIPLUNALIGULASKUTTHOGALHECLASY OSSENDAEAPAG FWUNAGOTHAGHANGAALCHUPTSPDL OSSENDAEAPAG FWUNAGOTHAGHANGAALCHUPTSPDL OFFIDER STANDARD FUNDAGOTHAGHANGAALCHUPTSPDL OFFIDER STANDAGA GOOD FOR THE THAGAND FOR THE THAGAND FOR THAGA		
			YLFISYLWINSKSELIRLINDALIGILASKHYTTHGIALICIASY GSREMAEAFAGE IRVILVAGOTHGWYGSAALCHLIVTETSDIL GSREMAEAFAGE IRVILVAGOTHGWYGSAALCHLIVTETSDIL YPMODITSKYWLLIMOGHLOWYTAATSLITTLAGKIPSEKTSY YPMODITSKYWLLIMOGHLOWYTAATSLITTLAGKIPSEKTSY PPPDPAWAGRITECESTLUKAGEPPESSKYQHSINGNALVERA SAUNSKLASILUKPAGNUGGOFQURSTHKYRLIALISKYCLA SASFSHEAWKHIGTVINALUTERUSVPQGARVILLIAMCDESSY APQUVARMLSYTETAGYSTERSTUKVALITLAGKYDYTON YUV TILALIR LAGOTVSEKWYKVIGTVINRODVGYAAKTVERALQ APACHMINIVKYGOTUGGEGLIALIGHGEBSSDIGTHLAGKEHL CSVPTAALLISTYLKFWINFPEVKSTIGDVLRSDGLUNDVEL CGVPTAALLISTYLKFWINFPEVKSTIGDVLRSDGLUNDVEL		
			YEFISYUNMANSELIPLUNALIGULASKUTTHOGALGICLASY OSERMALEAGES PKVUNAGOTBASKUSÇAALCILLAYETSIDL OSERMALEAGES PKVUNAGOTBASKUSÇAALCILLAYETSIDL OSERMALEAGES PKVUNAGOTBASKUŞÇAALCILLAYETSIDL OSERMALIAGES PKVUNAGOTBASKUŞÇAALCILLAYETSIDL OSERMALIAGES PKVUNAGOTBASKUŞÇAALCILLAYETSIDL OSERMALIAGES PKVUNAGOTBASKUŞÇAALCILLAYETSIDL OSERMALIAGES PKVUNAGOTBASKUŞÇAALCILLAYETSIDL OSERMALIAKUŞÇAALCILLAYETSIDL YETSIDL OSERMALIAKUŞTININALIKATICILLAYETSIDL OSERMALIAKUŞTININALIKATICILLAYETSIDL OSERMALIAKUŞTININALIKATICILLAYETSIDLO OSERMALIAKUŞTININALIKATICILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLO OSERVIYLIKINALIKATIONALIKATICILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETSIDLICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILLAYETTICAYILICAYILLAYETTICAYILICAYILICAYILICAYILIAYILAYILICAYILICAYILICAYILICAYILICAYIL		
			YEFISYUMSKSELIPLINGALIGILASKNYTHGIGALIGICASY OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFAG IFVUNGOTHOMYOSGAALCHLIVERSPOL OSROMAEAFACHUNGOTHOMYOSGAALCHLIVERSPOL GAALCHLIVERSPOL OSROMAEAFACHUNGOTHOMYOSGAACHUNGOTHOMY		
			YEFISYUNMANSELIPLUNALIGULASKUTTHOGLALECLASY SERMALEARGE PKYUNGOTHOGNAGOSALCHLIVERS DIL SORMALEARGE PKYUNGOTHOGNAGOSALCHLIVERS DIL SORMALEARGE PKYUNGOTHOGNAGOSALCHLIVERS DIL SORMALIA SERVINSA DILQUTYT PEOP FLIGSYULBILDICY PPEDPANGGULTEGLETILINGAGEPIES KYUNGSHANGAUPER SARSHENNEH ISTYINGAGEPIES KYUNGHANGAUPER SARSHENNEH ISTYINGAGEPIES KYUNGHANGAMDENSY LILIHIHDER JANDEN SERSI TUKAHLI ARKADITAN YUN APACHININYKAGYILDERGALI JANDENS PRI LÖMLITERAD APACHININYKAGYILDERGALI JANDENS PRI LÖMLITERAD OQRAVSTURISHIYIK KYUNGPEVENT QOVLANDAN YUTU OQRAVSTURISHIYIK KYUNGPEVENT QOVLANDAN YUTU OQRAVSTURISHIYIK KYUNGPEVENT QOVLANDAN YUTU OQRAVSTURISHIYIK KYUNGPEVENT QOVLANDAN YUTU OQRAVSTURISHIYIK KYUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK KYUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK KYUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK KYUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK KYUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA SICHAMIN YUTU OQRAVSTURISHIYIK YUNGPEVENTA YUTU OQRAVSTURISHIYING YUTU OQRAVSTURISHI		
			YEFISYUNBASELIPLINALIGILASENTTHOLALICIASY OSROMAEASAG IFVUNGOTOMOSOGAALCHUVTETSDIL OSROMAEASAG IFVUNGOTOMOSOGAALCHUVTETSDIL OSROMAEASAG IFVUNGOTOMOSOGAALCHUVTETSDIL OSROMAEASAG IVASTOLOGOTTOPOTOMOSOGAACCHULHUSTON ISALIHOSE STANDOOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUGOTOMOSOGAACCHULHUSTONICHULHUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUUT		
			YEFISYUNMANSELIRLINALINALIANLASHAYTHANGALECIASY SERMAEAFAGE PREVIANGATORASOGAALCIALKYERSDI. SERMAEAFAGE PREVIANGATORASOGAALCIALKYERSDI. SENSELAS YEROSTA SERVIANGATORASOGAALCIALKYERSDI. SENSELAS YEROSTA SERVIANGATORAS		
			YEFISYUNISKSELIPLUNALIGULASKUTTHOLIALUCLASV SERMMEAFREJE FRYUNGOTHOLIASKUTTHOLIALUCLASV VIMINDTSRUMLINDGHLOVTHANTSLITTLAGSTESSKTSV VIMINDTSRUMLINDGHLOVTHANTSLITTLAGSTESSKTSV VIMINDTSRUMLINDGHLOVTHANTSLITTLAGSTESSKTSV VIMINDSRUMLINGSRUMLINGGHLOSSKANALIRIA LISLIHUNGSFRILVSALDLAGFFESSKTSKANALIRIA ADQUARKLSTLETANTSIERETUKVALLAGKTANDTTNIVNO ADAGUARKLSTLETANTSIERETUKVALLAGKTANDTTNIVNO VIMINDSRUMLINGTVINLALIRIANDGHROSSKANALIRIA ADAGUARKLSTLETANTSIERETUKVALLAGKTANDTTNIVNO CORAVSTLESTVANTILIANDGHROSSKANALIRIANDGE CORAVSTLESTVANTILIANTUKSKANALIRIANDGHROS		
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				NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			FPLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENRNTLSWL
1			PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
[1	ILPPNOTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
			GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
			LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
1			RAAEL*HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLMIGP
ŀ			CIFNLVSRFISORLNCFIQASMQKHTDNIFHLCHV*YQSLRGNH SEAPEPRP
5856	1.73	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
	1		FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
1	1	1	IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
ì			VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVVMKQ
			LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
			SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
	l	ł	VMAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
1			PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
1			VMQSPLVGVTSTPGTGQSMFSPASIGOPRKTTLSPAGLDPFYTO
			GDSLTSEEH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
			LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPPQDSSKPVVAQGPGPAPGVGSAP
			PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1			PSSGVPTTPPQAGGPPPPPPAAVPGPGPGPKQGPGPKGGKMP
			GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
			GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
			LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
1			ALA*NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCIN
1			MPPQ MCWGRRPFRPNLGPHLKGAVCNRWDDFNEGPTGKGHCLN FAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
		2005	NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
			RTPIORTPHEIMRRESNRLSAPSYLARSLADVPREYGSSOSFVT
			EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
			HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
1 1			VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
1 1			YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQOTERNO
			SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
			YQGMLKLLFMKELEQIVKKYEAYRQALLTELENRKQRQQWYAQQ
			HGKNP
5860	2956	1.270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
			LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
1 1			SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI
1 1		i	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
1 1		J	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
1 1			NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
1 1	ļ		QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
1 1]		QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
1 1	1		VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
1			PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
1			CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV
1	1		KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
5861	2051	1305	KMGMKFVSDBHYDENEDDLVSHVDGSVISRREWYV
1 5001	2027	1303	EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
1	1		SEGEOGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
			LE*RMNSGSPARDNAPSQRFCTNLSEGLRPGISPSWREALYGCH
			AND TO AND THE PROPERTY OF THE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Jamino acid segment containing signal peptida La-Alanine, C.Cysteine, Debapartic Acid, Be Glutemic Acid, F=Phenylalanine, G=Glycine, H=Histidine, T=Isoleucine, K=Lysine, L=Leuccine, M-Methionine, N=Apparagine, P=Proline, O=Glutamine, R=Arginine, S=Serine, T=Thrconine, V=Valine, W=Tryptcphan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
			A
5862	1556	483	FPFGLIVAGELYSPDYNWFRGYVPLAKIT VONDDSKIVSLYDAG. PRSIACPLIFEPVOSTADDYFRGI LALLIAGWIYW. HALLOYDYW. BHLBFCOGFRELDHI, QLDVYLLFOALLGGFLACKFAETHIKSP GFVDPBBADATDFWLESSLAGSGELASFLITACONSYVEPHIK. LCSASZWILVYGUTESSLAGSGELASFLITACONSYVEPHIK. LCSASZWILVYGUTESSLAGSGELASFLITACONSYVEPHIK. ALGSASZWILVYGUTE. LCSASZWILVYGUTE. LGSASZWILVYGUT. LGSASZW
5863	2714	249	PEPSÄSSLEGLARPRETTYRGILMVIRFCLIFLYTVGILMDBARSECPON VIN SOOTPILLSROMAPOSILLYTS VEROCGLYEP BASKLICKSSOGNO TPOATRSLISKAVCKPVRCPAPVS ZENOT YTPRIGS YPVOGSVSP TPOATRSLISKAVCKPVRCPAPVS ZENOT YTPRIGS YPVOGSVSP CECHOPT 11,000 PVOG PVOG PROMORD THE VOG PVOG PVOG PVOG PVOG PVOG PVOG PVOG
5864	173	1013	PILISTOGISISIPOPELCEPGOGEPSAPSPCLYSFIMACSFTWG KLPBS1PSSBIACVLKRIKEP_CLUTPDLKPKGLIFFCTYAPGV KLPBS1PSSBIACVLKSKSCKFGKKSGKSFDVOAFF\S HMSLPSLCSGC/GLIPHLSSFSPFCSFG/FPQVPSG-/TESFFS MMSSDLPPPSACAPRCAPGAPSFORSHLASPPTYBFTSFFTMS SLCPHSVTSPFPPAQCFTLKKYAGAKGIVKVSAPFSLSQIF*RL GSFSSHIKIGSSSMLIMQOF
5865	568	1684	CLASPRANGENIA CHIVOCTE PER ATI SEPREGRATI CONCRETE LEVOCUCUO SERIO LOVICO CENTRA CENTR
5866	98	3197	ARPHYPAPPAMILSERGARANDENKODIOSPEKISKOKERRADI.DDI. KERVANTERBORVENKURKUNTUOOLIDHEAKOJA LAAKUPNA LITPPATTERWINTERGLEGGESILLIMIGAILIGELLYGIQATED DESODALI-GITULAAVITITGGESVYGAKASIKINES FRANVPO OALVIERBOBENQWARESVIVODIIVEIKSODIVRADLEI ISAHOG KUNSSILGISSERGYTYSERCTER VIKIKTEHITERSINTVEGTA ROVVANTODENWARI LATLASGEBVOGTA-LBIESHETOLITTOV CULTUMARDHENGENCHYSILANDEN GESTENTI-GORFTOTTATIONN TVAHMYPONGIHEATPERDSGTSPROSTENTI-GORTTOTTATIONN ROVKANTOREN VIKIKTHON GESTENTI-GORTTOTTATIONN OVKANTOREN VIKIKTHON GESTENTI-GORTTOTTATIONN ROVKANT

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
105:			Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILONHTEIVFAR
		Į.	TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
1		1	AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFENLKKSIAYTL
İ			TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
1	!	1	EAAESDIMKRQPENPRIDKLVNERLISMAYGQIGMIQALGGFFS
	1		YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
			VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
			GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
			YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRAKGGRCLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
		I	GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
	1		DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
1	1		ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
1			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
1	1		WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
1			GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
	1		TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
i	1		
1			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
			ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
1	l I		PDHCSDDA*QSCPAAAAPLQRQCDQSQGQITSPQSGNSGETFS
5868	2122		ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1]		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
	1		DPAGKLNQFRKNLRESQOLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
	i		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
ł			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5870	2122	833	
5070		633	LTAGASHTODASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLINGKHFQH
1			IQVCTPWLBAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
i			VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
1			LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
1 1	- 1		OGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
1 1	- 1		KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
1 1	1		YEEYGELQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
1 1			CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
1			L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
1 1	1	J	SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
1 1		J	FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
1 1			VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
1			
1 1		J	KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
1 1			DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
j	1		FLNTYGIQTOTPQOVEPIOIWPOOELVKAYLQLGINEKLGLSGR
ı ([1	PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
i 1			DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
1 1			LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS
1 1			PERLEPPKHSKVKRQSSTPSAPRLGQQPDVNISEWKDKPTHEIL
			QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

Predicted Predicted Predicted en				
muclootide location corresponding to first mullootide first mullootide first mullootide mul	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Location Corresponding				(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
Corresponding to first amino acid mediate of anino acid residue of anino acid residue of anino acid acid acid acid acid acid acid acid	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first mino acid mino ac				
### smino acid residue of smino acid smino a	1			P=Proline, O=Glutamine, R=Arginine
residue of amino acid sequence (http://pubplen.yr-tyrosine, X-Unknown, "s-Stop code, in acid sequence (http://pubplen.yr-tyrosine, X-Unknown, "s-Stop code, in acid colide deletion, 'Appealible nucleotide deletion, 'Appealible nucleotide deletion, 'Appealible nucleotide deletion, 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide insertion' in the 'Appealible nucleotide	1	amino acid		S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /-possible nucleotide deletion, Vepossible nucleotide insertion RESPUENCE (SALVANDE NUCLEAR PROVIDER NUCLEAR PROV	1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stcp
ASSOCIASIONERS AND SERVICIONES	1		sequence	Codon, /=possible nucleotide deletion.
ASSOCIASIONERS AND SERVICIONES		sequence		\=possible nucleotide insertion)
ISBNP\$LIPSCITUS THE MY THE MY THE ACCOUNT TO THE MY THE ACCOUNT TO THE MY THE ACCOUNT TO THE MY THE ACCOUNT TO THE MY THE ACCOUNT TO THE ACCO				AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
SEWOLLLOLLOPOUNG ROWLING CONTROL INFERTOR PICKWOOL LERRIPGICUL SHEEL SHE				HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVIQQELVIHIGWI
LERTPROLITYAGHHAPQQTLGSHTWISHNISELVEDTIGSHID PROPROLIVEMENTS (PORTS AND EXPONENTIAL PROPROSED AND EXPOSITION AN				
POYDGUVELLMOVS ULS REPERCE PORVIOLIBLE VERANESS OF ROOSE NAME REPORT POYDER PROPRIETS CHEMICAL PROPRIETS OF THE POYDER OF THE POYDER PROPRIETS OF THE POYDER PROPRIESS OF THE POYDER PROPRIESS OF THE POYDER PROPRIESS OF THE POYDER PROPRIESS OF THE				
FOOGRAKETERODINTS PYNTPPUGRROTCSTUTKANWALLIAES FOR				
5872 68 665 NUCHNICH STEERS CHRECOPELATOPH PPTYFF NIAL DEBELGCT ISTAL PADRY PERMICHPULSTOREN JOHN OFFITTIED LACASOPTHEMS TO SELTE ADDRY PROPERTY LEN THAN DEBELGCT ISTAL PADRY PERMICHPULSTOREN JOHN OFFITTIED LACASOPTHEMS TO SELTE ADDRY PROPERTY LEN THAN DEBELGCT ISTAL PADRY PERMICHPULSTOREN JOHN THAN DEBELGCT ISTAL PADRY PERMICHPULSTAN SELTE THAN DEBELGCT ISTAL PADRY PERMICHPULSTAN SELTE THAN DEBELGCT ISTAL PADRY PERMICHPULSTAN SELTE THAN DESTRUCTION OF THE PROPERTY OF THE PROPERTY AND SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTI ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTI ADDRESS TO SELTE ADDRESS TO SELT ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELDE ADDRESS TO SELTE ADDRESS TO SELTE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELTE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDRESS TO SELDE ADDR	1			PQYRQIVVELDMVVSIVL3RNPELEFQDKVDLDRLVKSAFNEFQ
5872 68 655 VOGWINFFYILTINGYTSERTSTCHRKCOPELDATJONETHYLTINGYTSERTSTCHRKCOPELDATJONETHYLTINGYTSERTSTCHRKCOPELDATJONETHYLTINGYTSERTSTCHANTONISLISSERTOBENIT/LIke INLAIDESSIGNIT/SERTSTCHANTONISLISSERTOBENIT/LIke INLAIDESSIGNIT/SERTSTCHANTONISLISSERTOBENIT/LIke INLAIDESSIGNIT/SERTSTCHANTONISLISSERTOBENIT/LIke INLAIDESSIGNIT/SERTSTCHANTONISLISSERTOBENIT/LIke INLAIDESSIGNIT/SERTSTCHANTONISLISSERTOBENIT/SERTSTCHANTONISLISSERTOBENIT/SERTSTCHANTONISCERTSERTORISCHANTONISCHERICKER/SERTSTCHANTONISCHERICKER/SERTSCHANTO	1	I	1	WANDED OF TO
NEAL DESIGNOTY SPEEL FADROY PERSPECTORY LLOTTORY LIGHT GOFFREY HIP OL LOCASION PRINCIPAL SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE TAPOVLSTANDOTY TO SUPERIOR SHANKSEN PROBENTY LIKE HELIALSANDO PRIVENTE STANDOTY TO SUPERIOR SHANKSEN THE HELIALSANDO PRIVENT SHANKSEN PROBENCY TO SUPERIOR SHANKSEN SHERLANDO PROBENTY SHANKSEN SHANKSEN SHANKSEN SHANKSEN SHANKSEN KURLIKUTE PITRI TYPE TO THE TOTTO SHANKSEN KURLIKUTE PITRI TYPE TOTTO SHANKSEN	5872	68	665	
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S973 2240 SG6 HERPEGEESSERTERSERVENSER SERVENS				GPCFYRIIPG\LCOGGDFTHHNGTGGKSLYSKEFDDENET/LVE
S873 2240 SO6 REPRESENSE SERVITANICOGU REPRESENSE SERVITANICOGUE REPRESENSE SERVITANICOGUE SERVITANICOGUE REPRESENSE SERVITANICOGUE CORRESTA SERVITANICOGUE REPRESENSE SERVITANICOGUE CORRESTA SERVITANICO SERVITANICOGUE CORRESTA SERVITANICO SER				TAPGVLSTANAGPTTNGSOFFICTAKTEDG+OHVVFGKUKDGMG
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LEFSGSLPPHAICLGDVDNDTLMELVVGDTSGKVSYTERDDSRP WLICSCCOMLTCVAVOD/CRKGKLLVAVASASWFHLEDLTFAK VLAASGHRELLGERPFVKFMITANTKVALISDDGCKEEL VVGTTDKVVARPREELGEPFHLTGGLVSLKNMKLEGGVDSLS VTLGFLCEFFKVSQCACATLCTKKNMKLEGGVDSLS VTLGFLCEFFKVSQCACATLCTKKNMKLEGGVDSLS				IFVF
WLICSCQMULTCVGGDVCNGGNLLVAVSASGFRLEDLTPAR VLAASGHRINTLIGERGBYPFGGNIFANTFULISDIDDDCCEEL VVGYTDRVVAAFRBELGEBPHILTGQLVSLKXMILGGQVDSILS VTLGDLLGELMVSDCGCAVALLLLCVMKNOTSPASGBYTDG VTLGDLLGELMVSDCGCAVALLLCVMKNOTSPASGBYTDG	5875	296	1848	
VLDASGHHRTLIGERGREVERGHIPATTKYMLISDIDGDCCREL VVGTTDKVRAFRWEELEGDPHILTGQLVSLKNMLEGQVDSLS VTLGPLGLEELMVSQRCCAYAILCTWKKDTGSPFASBSPFTDS	1 1	i		
VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				
VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASBGPTDGS	1		1	
	i I			
/ SGDFSUPRRGMAPHINF I PUQBUHSPNNQHQT\SHGTESSGS	i I			
		Ì		

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	GLFALCTLDGTLKLMREMERADKLLWSVQVDHQLFALEKLDVTG
			NGHEEVVACAWDGQTY11DHNRTVVRFQVDEN1RAFCAGLYACK
			RGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
			TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPOASRIPPS
			WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKO
5876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAULKKIFGDHPIPQYEV
1	******		NPRTTBILHHLSERNRVRORDVYLVIEDLKQKASEYESEAKYIQ
1			DLIMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
			AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV
	1		KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
			GARGOL DA ROUD FOR 1127 TO THE PROPERTY OF THE PARTY OF T
			SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
5877	2030	1907	LMP\N7SHCSK*RIBEAK\RELA\SIEAELTRRVS\MMEL
1 3377	2030	1307	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
1		ĺ	LSRBLIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA
I		l	LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
1			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
			PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
5878	950	21.13	CPCSTVS/NGSQMTCR*INIILILQKSVCEL
3070	350	2113	GLWKCHQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
i		ĺ	RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP
1			ISIKNARVSQHYKASLTATFNLFPBAKFAVVLEEDLDIAVDFFS
	ł		FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
			LGWVLRRSLYKERLEPKWPTPEKLWDWDMWMRMPEQRRGRECII
			PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
			KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR
			MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLPRKKNHFLVV
5879	3	004	GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
30/9	, ,	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
Į.			GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
			AIAMVRFYMEKGTHRGLYESIQKTLKFFQTFALLEIVHCLIGIV
			PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
			BITRYSFYFFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
1			AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
			YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
5880	2752		NNKNKQLCEISWIVWFLKI
5000	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA
1			SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
1			*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
	1		CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP
1			DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKKQRYN
1			ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC
			AEVKQBLAASRTARDAALBRVQMLEQQILAYKDDFMSERADRER
1			AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA
1			ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
			CLQCFSDEQGEELLRHVABCCQ
5881	26	441	GGIHPSPTEAPRAQHLIMDCTWRILFLVAAATGTHAQVQLLQSG
1			SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD
			LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV
			HHCATDTV
5882	2407	2216	SGCVEMLYSHSLEYN PEWISVQSAVAPAQLALNSDGDL*LHSGE
			RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR
1 1			HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER
			MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLENRQAVRGKLG
1			ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE
			ARGTAACADVRGVLDRLRVKAVTKIRRFILQKIYSFRKPMINYQ
			IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR
1			SYLGRIMKVQYERVARKDDLMGVEDTAKKGFFSKPSLRSRNTIF
	ļ		TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL
1			LDNSCREYLFICEFFVVSGPAAHDLFEAVNGRTLSMTLKHLDSY
			LADCYDAIAVPLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

SEO	Predicted	Predicted end	1
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
	i		SINQTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLI
1			MINYDAMI CUTAN PARDA A DOUTTING DO CA AND STREET OF THE
1		}	NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
1	i		PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
1			SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L SQPQLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	SQFQDRADPARABBINIAHDEVELKKAKPNF
1	i -	13/4	EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG
1			CERKKGQRWGSLERRGMQAMBGEVLLPALYEEEEEEEEEEE
i			EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
1			BETRELAGQHEDDSLELCGLLEDERLASAQQAEVFTKQIQQLQG
1			ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
í			ATBHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
			MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALQESNS
1			SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLED
ì			DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEELQHHRQVSEE
	ł i		EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPFIPPSSPCLL*A
5884	4261		LVVISALLWCWWAETSS
2004	4451	2522	GVLARASARLRVPLTGVRACABPEVGAEPAKVAGAAEPDEDGGR
i			SRLRDCGDYTPSERLGPKGANLWFQGAIPAAIATAKRSGAVFVV
1			FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
}			SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM
1			HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
			IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE
			RLTKKLEBRREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE
			ELTKRMLEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
1			EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF
			TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
			KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
i l	i		TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLBKRGDDFKKEGKIYRLRTQDDGEDENNTW
5885	900		NGMSTQQM
3003	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
]			IYWPRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
	1		YLQIDEEEYGGTWELTKEGFWTSFA/IVHGHLDHLLHCHPL*LM
5000			VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKOPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
! [i i		GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
			EVLLEALFLTVDPYMRVAAKRLKRGDTMMGQQVAKVVESKNVAL
	1		PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
i 1	1		MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
			KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEETLKKASPDGY
			DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
			PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
			D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
			NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE
			RPDRCHPGGDDRGPQLHRGSPG/SPSBLSRRPGPPGLPGLOGPP
I			PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
ł			ACSVFVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
			FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY
		J	VSFTTKLDIPTAAKYRYGVPLQTSDSFLRFPSSLTSSLCTDNNP
- 1	l		AAFLVNQAVKCTRKINLEQCEEIRALSMAFYSSPEILRVPDSRK
			KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
1	1		LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
- 1	į.		ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGDLTI
			LHSTTEQDCLALEGVRTPVLFGYTMOSGCKLRLTGALPCQLVAO
	i i		KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
- 1	1		DSCQLPGALVIEVKWTKYGSLLNPQAKIVNYTANLISSSFPEAN
- 1	1		SGNERTILISTAVTFVDVSAPARAGFRAPPAINARLPFNFFFPF
- 1	Ĭ.		V

WO 01/53312

PCT/US00/34263

SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serinc, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSARADWSPG
			LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
1			CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDFIH
j			GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
1			SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1			PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
	1		QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
	1		IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
			DNELRICARDKEVGNLYDMFHTRNSLHRRAYCHKVGNIIDTMIT
J	J		DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
1			YSTDPKLKDAREILKQIEYRNLFKYVGETOPTGOIKIKREDYES
1			LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
1			FYCKTAPNRAIRITKNQVSQLLP\EXFAEQ\LIRVYCKKVDRKS
			LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPOKKGW\
l			NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPROAPEGRSGRPRDLDPYPPOVFPPRPDRVAT
		/	VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKOVVSKIKEET
1			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
			FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
1			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
			SATHYVABLNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
			AABGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
1	ľ		DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLOSGTEAACRS
			GRPDPRPASAAGGHAGERMSORDTLVHLFAGGGGGTVGATLTCP
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPINLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KQKLLEYKTASTMENDEESVKBASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEBGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQUVLGHLRGPA
			DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
			TPDELLSAVWTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1 1			AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
			CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
			FGISREKODTFALASOOKAARAOSKGCFOAEIVPVTTTVHDDKG
			TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSOVS
			DGAAAILLARRSKABELGLPILGVLRSYAVVGVPPDIMGIGPAY
	1		AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
			*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
	!		PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEFT
- 1	ŀ		CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
			MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
- 1	I		DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
j	ļ		GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
	ŀ		NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
			TAVKWMIBQOMNRWFNHENYGLEPONKYIMKEPVLNDDVPSRLL
			CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

Deginning corresponding toation corresponding to first samina acid samina cide	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note location corresponding correspond				
Contresponding Coffeeponding Coffeeponding Cofficial Endition of first anino acid cofficial Endition of committee Coffee Cofficial				
corresponding to first amino acid and conduct of the conduct of th	,			
to first amino acid am				
amino acid residue of amino acid amino acid sequence WT:Pypopholin, T-Tyrosinine, X-Unknown, *-Stop Coden, /-possible nucleotide deletion, ACRICANO, T-Pyposible nucleotide indertion LENSINYVERNWISITYSTFFAHIDISTIACTGRIQUESISPT ACRICANO, /-possible nucleotide indertion LENSINYVERNWISITYSTFFAHIDISTIACTGRIQUESISPT ACRICANO, /-possible nucleotide indertion LENSINYVERNWISITYSTFFAHIDISTIACTGRIQUESISPT ACRICANO, /-possible nucleotide indertion LENSINYVERNWISITYSTFFAHIDISTIACTGRIQUESISPT ACRICANO, /-possible nucleotide indertion STYPELVOROROMANIPTYCOLOGISESTEMBOLITERISTICATION (INC.) SYPELVOROROMANIPTYCOLOGISESTEMBOLITERISTICATION (INC.) WINTYMEOGRAPHANIPTYCOLOGISESTEMBOLITERISTICATION (INC.) ENERGISPTUCHUS (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICALOGISESTEMBOLITERISTICATION (INC.) LENSINYENDYLEDICATION (INC.) ESPECIAL COLOGISTICATION (INC.) LENSINYENDYLEDICATION (INC.) LENSINSHIPPORTATION (INC	1			
residue of mino acid sequence (Coden, /-possible nucleotide deletion) equence (Coden, /-possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide deletion) (Possible nucleotide) (Possib				
amino acid sequence Codon, /-possible nucleotide injection LEDSLYVERNAMUSLIYIYFFAHLDESTIACHIGFGSTSTFT ARLAMANVIRTHYTYFFAHLDESTIACHIGFGSTSTFT ARLAMANVIRTHYTYFGALCLESSTFTDESTIACHIGFGSGSTSTFT ARLAMANVIRTHYTYGGALCLESSTFTDESTIACHIGFGSGSGTTLANGUSGALCHIGFGGGGGTTLANGUSGALCHIGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				S-Serine, T-Threonine, V-Valine,
Sequence			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
LEBSLAWAYENNUSLIYAY FERMALDASTIA.CRILTOPEASIPS ARALQARAY TRYPROGLICLOPES AND LOPES OF CHARLAND ARALQARAY TRYPROGLICLOPES AND LOPES OF CHARLAND ARALAGA AND ARALAGA ARA		amino acid	sequence	Codon, /-possible nucleotide deletion,
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BRTELOPTISABALYTAL VWOGKKO EDVIGASVRETLIFILDELSE RÖNNOPPLAGESTESAD TUMARKYTHLODDRIVLEGELALISM ROTLETO'S PEORE SABATUKA VOGKKOL EPULODRIVLEGELALISM ROTLETO'S PEORE SABATUKA (OCCULATE, PPLOGROGO SER ROKLESI EDER SEBELATILSES LANAVYRAK KOLESE, PPLE POO KPULEVAGERKULTSAS, PPUNKOVRIGANI TOCVLSADVPRAYS RIKKOMETALLOGOPEVATATETRAK, PEGELOPES CONSENSI HAR DIT'N KWRII SEDI SERTITEO'S VATAV (DEGILOGORISM) TVRQIALERICA, PLADRYPROVED PEGE SERRAGORISMORISMORISMORISMORISMORISMORISMORISM	1			
RQ\NCPELAGETESLADYUMGALYPILLODRYLPERICALISM PGTLETGY RPGG, ARARILLAUG, GCVLALAS, PYLLOGROPGESA SCRULED LEPER ELATISES LANGUARIAS, PYLLOGROPGESA SCRULED LEPER ELATISES LANGUARIS COLLEGE PPLE PGG NEPULAVAGERISM, TESALPYENDE LONGUARIS LANGUARIS COLLEGE LONGUARISM, TESALPYENDE LONGUARISM, VERGUARISM, TESALPHANDE LONGUARI	1			
POTLETO\S PCOR\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1			
SORGIAS-PIEPERS-LATIASSEZ-LAMA/THAWRICLESS-PPER-POQ NPVLPWAGES-BULLTISSA_PPUNNPLAGNIC TOUCHAGAD PER-RYS RILGOMETLYL-COPTIEVERYTHTEVALA-DEGITPOG-CONSYST-LEA- DITA (AWRES-IS-DI-GERTTIFOG/CATACTACH-DIS-COLORED-LEA- DITA (AWRES-IS-DI-GERTTIFOG/CATACTACTACTACTACTACTACTACTACTACTACTACTA	1			
NPULVAGENRULTTSALPYVANDRIANI TGOVLSADVPARYS RLEGGHFULDOGTFORTMATERSAL REGISTRES CONSKYLLINA DITA KRENTA ER DI SERTITROGA TRATO (DI GOLLARGE PULLO) TVRQLACERICA PLADRIPARO PE CONSTRUCTOR CONSCILLA KANDELKENDOCKVORSCOVVOSCOLINA DIDEN ER SELEMINATE ESCHATINADO (EL TRATOTTO CONSTRUCTOR DE CONST	1	1		
RLROWHTLYLCOTDEVGTATETKAL\EBGLITFGET.CDYFHITHA DITY\RWINISED IGRRTTPGO\TC\TKT\OT\GTG\TC\TC\TC\TC\TC\TC\TC\TC\TC\TC\TC\TC\TC\	1			
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DITY NEWTHER DISCRIPTION OF THE THOO THE CONTROL OF				RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
TVROBLAGENCAR PLADRY USON CFCC YESSAROD CINCCIKLI. NAVELKEPC CVCRSCPLVOS SOBILE ILD ENE RESEAUGRTL POSDAT PRACTICAL PROGRAM P				
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PM_AEDMYPESLUPPSSALGABENYTL_VSHLATETLIYEDG K\PSIKSRIVGYEDM\AHDIOTIG PDDI SEYT_LLYT PSGK\DSA FSHTDLLENNS\S\LABLICATE\AHDIOTIG SEYT_LLYT PSGK\DSA FSHTDLLENNS\S\LABLICATE\AHDIOTIG\AHDIOTIG\ATGRES\S\LABLICATE\AHDIOTIG\AHDIOTIg\AHDIOTIg\AHDIOTig\AHDIOTig\AHDIOTig\AHDIOTig\AHDIOTig\AHDio				
K\SBISBOYGUFEDM\AUDTGIPPDISFYI_LYIPPBGK\DSA FSWTDLLIANDS\BLANNLEWFINR\GMFUSFFGG\YYPEMV LIPPDORILA\HYTLEGHTHG\LEEVISIDERSILTISKE GNGTI\GVBEFW\KRIKSBADRGRAFTVIELAVELARLISHUL GPWPTYSRITIOOGLOEPPROFESLLITISTLITISKELTAGUIGTYSP				
PSWTDLLEANN, SLELABLICAR TICKNO, OWNYSER FOR TYPERWY LITERORELLA HAVIELECKERU, DELEGERA HELEGERA LETTA, KE GNOZY T, OWNSEWN, KELKINSBADNORAGT VITGLAVNI LANLL. SWILL OPWINTVINSKI TLOOLOLOLPAPROE, LILLTIFILLTIPARO (LOTVS)	1 1	ı		
LTPDOQRIAS/AVTLEIGHYN(\LEKYA:RDAGS'ILTIS\RH GNQYI\QVNEFW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPTMPTVSATIQALGLEPPRGCSILINTELCTLPRAGURGTVSP	1			
LTPDOQRIAS/AVTLEIGHYN(\LEKYA:RDAGS'ILTIS\RH GNQYI\QVNEFW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPTMPTVSATIQALGLEPPRGCSILINTELCTLPRAGURGTVSP	1			FSWTDLLLKNKS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				
QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				
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		L		or Summer Supplied or consider the Late of

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence	Loquonov	\=possible nucleotide insertion)
			LMDEVTKOGNIVRELKAOKADKNEVAAEVAKLLULKKOLAVAEG
1			KP?EAPKGKKKK
5897	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINGRGIHGE
1			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEREIAMAVTAWEKGLESLPPLRPQQ
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS
		l	RLROWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
			DIY\RWFNISFDIFGRTTIPOO\TKIT\ODIFOOLLKRGFVLOD
	i		TVEOLRCEHCARF\LADRFVEGVCPFCGYEEARGDOCDKCGKLI
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTF*E
		ļ.	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
		ŀ	FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1	ł		K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPENV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
	ŀ		GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
		ļ	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDOIESLRQRFGGGGAKTSPKPAVVETVTTAKPQQIQA
			LMDRVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPEAPKGKKKK
5898	2967	86	HPSLLGAIPFYPFPSSPWPPPLYLFWNSHRKSRHFINGRGINGE
1			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATBLQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDFAYLPEELSALHSW
			FOTLSTQ\EPCOR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
Į.		l	EGKGLSPIEPEEELATLSEEBIAMAVTANEKGLESLPPLRPQQ
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1		•	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1			TVEQLRCEHCARF\LADRFVEGVCPFOGYEEARGDQCDKCGKLI
1			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAOFITPFFGFREWPSKPRMO*TRDLK\WGNPGTP*E
			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDIYQ
1			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
ł			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
ĺ			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPS?LRAAMALSDVDVKKQIKHMMAFIEQ
	-50	1	BANEKABBIDAKABBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE
			QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
			EVYQGLEDKLVLQGLERLLEPVMIVRCRP\QDLLLVEAAVQKAI
1			PEYMTISQKHVKV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
L			TLESKLDLSAKQKMPEIRMALFGANTNRKFFI
5900	64	1409	KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK
1			GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
1			KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
1			KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI LWNABIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
1			VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGETAYTKLA
1			LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL
			The state of the s

SEC	Predicted	T 9 11 1 1 1 1	
		Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
: CM	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of		
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QKAPERFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
	1	i .	/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
1			NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
1			
5901			NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
		ł	KTHLETVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
		1	SCDKOFTSVDDLOKHLLDMHTFVFFRCTLCQRVFDSKVSIQLHL
			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
		I	CIFCGESFGTEVBLQCHITTHSKKYNCKFCSKAFHAIILLEKHL
			REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
l l			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
1			AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMCTHLGPVKFYM
1			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEREFL
1	1	1	BHCOMEPDLENSLTGFRCVVCMQTVTSTLELKIHGTFHMOKTGN
1		1	GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLWKLDINGLPYGL
1	1	1	Charles and a partition of the partition
1		I	CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
i	1	1	KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
			QVSPMPRISPSQSDEKKTYQCIKCQMVFYNENDIQVHVANHMID
1	1		EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
	l .		FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
1	l.		HSS
5902	712	209	LKNRRRSRPSIRCSIGSTSVSRWLTSLFTYLDHTADVO*V*REF
3302	/12	203	
1	I		IPLKPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
		l	VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
1	l .	l	EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
			PALFALSAVPGGAASPMPPSGLRLLPLLPLLWLLVLTPGRPAA
	l .		
	j.	ł	GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
1	1		LPEAVLALYNSTRDRVAGESABPEPEPEADYYAKEVTRVLMVET
1	1	ŀ	HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
1			RQWLSRGGEIEGFRLSAHCSCDSRDNTLOVDINGFTTGR\RGDL
1	1	1	ATTHGMNRPFLLLMATPLERAGHLQS\SRHRQAL\DTNY\CFSF
			HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
			CDCDVCMCCDCC/ VNC - NDIFKKDD (GW \XXI \NE \FKGINARFC \L
i	l .		GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIRNAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
			ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
1			RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
	1		HEKWYOKFLALEERKKESIOIWKTKKOOKREEIFKLKEKADNTP
1	l		VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKCASOL
1			
1			KEEEBKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKEI
1			REKAEKAEKRKNAADEISRFQERDLHKLELKILDROAKEDEKSQ
			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
1			ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRT GELLAPAAPFDKKOGRENWTVAFAP
1			DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRL3R
1			
1			QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVFEKQSRCVNIEWH
			RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
1 1			TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
1			SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
i			WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
1			SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSEFNLM*SI
1			
1			WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
1			KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
1			LLIFR: *NCI * TYS * IIDPFYIQMTYDRG * FGKNKMVKF * FIEM
1 1			*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
1			QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
1			REGGL*YLTLFISVYFS*LVFGINGFOYSFVVKLHCLYFVFRLI
1 1		1	
			FKLTFMRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*
1			
			YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM